

```

OS Synthetic.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /*tag= a
FT /note= "contains phosphorothioate internucleotide
FT linkages"
XX
XX WO9823294-A1.
XX
XX 04-JUN-1998.
XX
XX 26-NOV-1997; 97WO-US022017.
XX
XX 26-NOV-1996; 96US-00757024.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1998-322464/28.
XX
XX Treating respiratory disease with antisense sequences directed against
XX adenosine or bradykinin receptors - with localised delivery to the
XX respiratory system, suitable for long term treatment of asthma, adult
XX respiratory distress syndrome etc.
XX
XX Claim 12; Page 8-24; 47pp; English.
XX
XX Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
XX human adenosine A1 receptor, the design of which required the secondary
XX structure of this targets mRNA. The adenosine receptor mRNA secondary
XX structure was both analysed and used to construct antisense
XX oligonucleotides containing a phosphorothioate backbone. Once the
XX antisense molecules are created they can be used to target their
XX predetermined target, thus causing the gene product to decrease. The
XX antisense oligonucleotides were targeted to specific mRNA regions
XX containing either a junction between the intron and exon, or where they
XX may overlap the initiation codon. The receptor is a member of the G-
XX protein coupled family of cell surface receptors that have 7-
XX transmembrane segments. These oligonucleotides can be used to treat or
XX prevent conditions associated with bronchoconstriction and/or lung
XX inflammation in humans or other animals e.g. asthma, pulmonary disease,
XX allergy, emphysema and cystic fibrosis
XX
XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GCGGGGC 8
XX Db 3 GCGGGGC 9
XX
XX RESULT 551
XX AAV47410
XX ID AAV47410 standard; DNA; 10 BP.
XX
XX AC AAV47410;
XX
XX 10-NOV-1998 (first entry)
XX
XX Antisense oligonucleotide 910, targeting adenosine A1 receptor.
XX
XX Secondary structure; mRNA; phosphorothioate backbone; G-protein;
XX bronchoconstriction; lung inflammation; asthma; pulmonary disease;
XX allergy; emphysema; cystic fibrosis; ss.
XX
XX Synthetic.
XX Homo sapiens.

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XX
FH Key Location/Qualifiers
FT modified_base 1..10
FT /*tag= a
FT /note= "contains phosphorothioate internucleotide
FT linkages"
XX
XX WO9823294-A1.
XX
XX 04-JUN-1998.
XX
XX 26-NOV-1997; 97WO-US022017.
XX
XX 26-NOV-1996; 96US-00757024.
XX
XX (UYEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1998-322464/28.
XX
XX Treating respiratory disease with antisense sequences directed against
XX adenosine or bradykinin receptors - with localised delivery to the
XX respiratory system, suitable for long term treatment of asthma, adult
XX respiratory distress syndrome etc.
XX
XX Claim 12; Page 8-24; 47pp; English.
XX
XX Sequences AAV46501-V47446 are anti-sense oligonucleotides that target the
XX human adenosine A1 receptor, the design of which required the secondary
XX structure of this targets mRNA. The adenosine receptor mRNA secondary
XX structure was both analysed and used to construct antisense
XX oligonucleotides containing a phosphorothioate backbone. Once the
XX antisense molecules are created they can be used to target their
XX predetermined target, thus causing the gene product to decrease. The
XX antisense oligonucleotides were targeted to specific mRNA regions
XX containing either a junction between the intron and exon, or where they
XX may overlap the initiation codon. The receptor is a member of the G-
XX protein coupled family of cell surface receptors that have 7-
XX transmembrane segments. These oligonucleotides can be used to treat or
XX prevent conditions associated with bronchoconstriction and/or lung
XX inflammation in humans or other animals e.g. asthma, pulmonary disease,
XX allergy, emphysema and cystic fibrosis
XX
XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GCGGGGC 8
XX Db 1 GCGGGGC 7
XX
XX RESULT 552
XX AAV35934/c
XX ID AAV35934 standard; DNA; 10 BP.
XX
XX AC AAV35934;
XX
XX 26-AUG-1998 (first entry)
XX
XX Primer used in RAPD assay of the invention.
XX
XX Rapid amplification of polymorphic DNA; RAPD; allele; breeding programme;
XX muscle fibre composition; Duroc pig; meat quality; PCR primer; ss.
XX
XX Synthetic.
XX Sus sp.
XX
XX WO9815837-A1.
XX

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XX PF 17-SEP-1998; 98WO-US019419.
XX XX
XX PR 17-SEP-1997; 97US-0059160P.
XX PR 09-JUN-1998; 98US-00093972.
XX XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 1999-229400/19.
XX XX
XX PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX PT vasoconstriction.
XX PS Disclosure; Page 41; 120pp; English.
XX XX
XX CC The specification describes antisense oligonucleotides (AA52869-X55271)
XX CC directed against at least 2 mRNAs selected from target genes, coding and
XX CC non-coding regions of RNAs corresponding to target genes, gene initiation
XX CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX CC end and the juxta-section between coding and non-coding regions and all
XX CC segments of RNAs encoding proteins associated with one or more diseases,
XX CC conditions or mixtures. The antisense oligonucleotides may be derived
XX CC from sequences AA5272-74. These multiple target oligonucleotides
XX CC (specifically AA55180-271) can be used for the antisense treatment of
XX CC diseases and conditions. Typical diseases and conditions are those
XX CC associated with impaired respiration and inflammation, including lung
XX CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX CC acute asthma, allergies, asthma, impeded respiration, respiratory
XX CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX CC well as all types of cancers which may metastasize or have metastasized
XX CC to the lungs, including breast and prostate cancer
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGGC 8
Db |||||
2 GCGCGGC 8

RESULT 555
AA53768
ID AA53768 standard; DNA; 10 BP.
XX AC AA53768;
XX XX
XX DT 05-JUL-1999 (first entry)
XX XX
XX DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX KW Antisense oligonucleotide; multiple target; antisense treatment;
XX KW impaired respiration; inflammation; lung disease;
XX KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX KW acute asthma; allergy; asthma; impeded respiration;
XX KW respiratory distress syndrome; pain; cystic fibrosis;
XX KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX KW prostate cancer; ss.
XX OS Synthetic.
XX PN W09913886-A1.

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XX PD 25-MAR-1999.
XX XX
XX PF 17-SEP-1998; 98WO-US019419.
XX XX
XX PR 17-SEP-1997; 97US-0059160P.
XX PR 09-JUN-1998; 98US-00093972.
XX XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 1999-229400/19.
XX XX
XX PT New antisense oligonucleotides used in treatment of, e.g. pulmonary
XX PT vasoconstriction.
XX PS Disclosure; Page 41; 120pp; English.
XX XX
XX CC The specification describes antisense oligonucleotides (AA52869-X55271)
XX CC directed against at least 2 mRNAs selected from target genes, coding and
XX CC non-coding regions of RNAs corresponding to target genes, gene initiation
XX CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
XX CC end and the juxta-section between coding and non-coding regions and all
XX CC segments of RNAs encoding proteins associated with one or more diseases,
XX CC conditions or mixtures. The antisense oligonucleotides may be derived
XX CC from sequences AA5272-74. These multiple target oligonucleotides
XX CC (specifically AA55180-271) can be used for the antisense treatment of
XX CC diseases and conditions. Typical diseases and conditions are those
XX CC associated with impaired respiration and inflammation, including lung
XX CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
XX CC acute asthma, allergies, asthma, impeded respiration, respiratory
XX CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
XX CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
XX CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
XX CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
XX CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
XX CC well as all types of cancers which may metastasize or have metastasized
XX CC to the lungs, including breast and prostate cancer
XX SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGGC 8
Db |||||
3 GCGCGGC 9

RESULT 556
AA53787
ID AA53787 standard; DNA; 10 BP.
XX AC AA53787;
XX XX
XX DT 05-JUL-1999 (first entry)
XX XX
XX DE Human adenosine A1 receptor antisense oligonucleotide fragment.
XX KW Antisense oligonucleotide; multiple target; antisense treatment;
XX KW impaired respiration; inflammation; lung disease;
XX KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
XX KW acute asthma; allergy; asthma; impeded respiration;
XX KW respiratory distress syndrome; pain; cystic fibrosis;
XX KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
XX KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
XX KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
XX KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
XX KW prostate cancer; ss.
XX OS Synthetic.
XX PN W09913886-A1.

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XX WO9913886-A1.
PN
PD 25-MAR-1999.
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
XX (UVEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
XX Disclosure; Page 41; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AA52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AA55272-74. These multiple target oligonucleotides
CC (specifically AA55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 1 GCGGGGC 7

RESULT 557
AA54553/c
ID AA54553 standard; DNA; 10 BP.
XX
XX AA54553;
XX
XX 05-JUL-1999 (first entry)
XX
XX Human adenosine A2b receptor antisense oligonucleotide fragment.
XX
XX Antisense oligonucleotide; multiple target; antisense treatment;
KW impaired respiration; inflammation; lung disease;
KW pulmonary vasoconstriction; inflammation; allergic rhinitis;
KW acute asthma; allergy; asthma; impeded respiration;
KW respiratory distress syndrome; pain; cystic fibrosis;
KW pulmonary hypertension; pulmonary vasoconstriction; emphysema;
KW chronic obstructive pulmonary disease; leukemia; lymphoma; carcinoma;
KW colon cancer; breast cancer; lung cancer; pancreatic cancer;
KW hepatocellular carcinoma; kidney cancer; melanoma; hepatic metastasis;
KW prostate cancer; ss.

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XX Synthetic.
XX WO9913886-A1.
PN
XX 25-MAR-1999.
PD
XX
XX 17-SEP-1998; 98WO-US019419.
XX
XX 17-SEP-1997; 97US-0059160P.
PR 09-JUN-1998; 98US-00093972.
XX
XX (UVEC-) UNIV EAST CAROLINA.
XX
XX Nyce JW;
XX
XX WPI; 1999-229400/19.
XX
XX New antisense oligonucleotides used in treatment of, e.g. pulmonary
PT vasoconstriction.
XX
XX Disclosure; Page 43; 120pp; English.
XX
XX The specification describes antisense oligonucleotides (AA52869-X55271)
CC directed against at least 2 mRNAs selected from target genes, coding and
CC non-coding regions of RNAs corresponding to target genes, gene initiation
CC codons, genomic flanking regions, intron-exon borders, the 5'-end, the 3'-
CC end and the juxta-section between coding and non-coding regions and all
CC segments of RNAs encoding proteins associated with one or more diseases,
CC conditions or mixtures. The antisense oligonucleotides may be derived
CC from sequences AA55272-74. These multiple target oligonucleotides
CC (specifically AA55180-271) can be used for the antisense treatment of
CC diseases and conditions. Typical diseases and conditions are those
CC associated with impaired respiration and inflammation, including lung
CC diseases, pulmonary vasoconstriction, inflammation, allergic rhinitis,
CC acute asthma, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, pulmonary hypertension,
CC pulmonary vasoconstriction, emphysema, chronic obstructive pulmonary
CC disease (COPD), and cancers such as leukemias, lymphomas, carcinomas e.g.
CC colon cancer, breast cancer, lung cancer, pancreatic cancer,
CC hepatocellular carcinoma, kidney cancer, melanoma, hepatic metastases, as
CC well as all types of cancers which may metastasize or have metastasized
CC to the lungs, including breast and prostate cancer
XX
XX Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGGC 9
Db 9 GCGGGGC 3

RESULT 558
AAZ22665/c
ID AAZ22665 standard; DNA; 10 BP.
XX
XX AAZ22665;
XX
XX 04-JAN-2000 (first entry)
XX
XX T14 primer for amplification of fungal genomic DNA.
XX
XX commercial; assay; test; fungal pathogen; crop protection; cucurbit;
KW primer; PCR; RAPD analysis; isolate; food crop; ss.
XX
XX Synthetic.
XX
XX EP950719-A2.
XX
XX 20-OCT-1999.

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XX PF 10-MAR-1999; 99EP-00104751.
XX PR 16-MAR-1998; 98US-0078103P.
XX PR 22-FEB-1999; 99US-00255432.
XX PA (UYCL-) UNIV CLEMSON.
XX PI Keinath AP, Somai BM, Dean RA;
XX PI WPI; 1999-582557/50.
XX DR Detecting a pathogenic fungus in cucumbers, pumpkins and gourds using
XX PT recombinant techniques.
XX PS Example 3; Page 8; 19pp; English.
XX CC This is a commercial oligonucleotide primer for the PCR-based RAPD
XX CC analysis of fungal isolates of Didymella bryoniae and Phoma species. The
XX CC new method may be used to distinguish D. bryoniae from non-pathogenic
XX CC Phoma species fungal infections in Cucurbits (i.e. cucumbers, pumpkins,
XX CC watermelons, gourds, cantaloupes, squashes and related plants). The new
XX CC method of detection of D. bryoniae and Phoma species infections allows
XX CC rapid diagnosis even before symptoms are visible as compared to prior art
XX CC methods which involved growing pure cultures of the pathogens from the
XX CC infected plants and identifying them under the light microscope. The
XX CC method leads to the early treatment of the infected plants with
XX CC fungicides resulting in an increased chance of saving the infected food
XX CC crops
XX SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GCGGCAT 13
DB 8 GCGGCAT 2
RESULT 559
AAA33221
ID AAA33221 standard; DNA; 10 BP.
AC AAA33221;
XX DT 28-JUL-2000 (first entry)
XX DE Low adenosine antisense oligonucleotide SEQ ID NO:910.
XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX KW phosphorothioate; impaired respiration; inflammation; allergy;
XX KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
XX KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX OS Homo sapiens.
XX XX WO200009525-A2.
XX PN 24-FEB-2000.
XX PD 03-AUG-1999; 99WO-US017712.
XX PF 03-AUG-1998; 98US-0095212P.
XX PR (UYEC-) UNIV EAST CAROLINA.
XX PA Nyce JW;
XX PI

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XX WPI; 2000-205971/18.
XX DR New antisense oligonucleotides useful for treating e.g. pulmonary
XX PT vasoconstriction, inflammation, allergies, asthma, hypertension,
XX PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
XX PT cancers.
XX PS Claim 18; Page 379; 1343pp; English.
XX CC The present invention describes a new composition comprising an antisense
XX CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
XX CC nucleic acids involved in bronchoconstriction, allergies, and/or
XX CC inflammation. The ON can have antiinflammatory, antiallergic,
XX CC antiasthmatic, cytotatic and analgesic activities. The compositions are
XX CC useful for the treatment of diseases associated with inflammation,
XX CC impaired airways, including lung disease and diseases whose secondary
XX CC effects afflict the lungs of a subject. They can be used for treating
XX CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
XX CC impaired respiration, respiratory distress syndrome, pain, cystic
XX CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
XX CC pulmonary disease (COPD), and cancers such as leukemias, lymphomas,
XX CC carcinomas, and cancers which may metastasize to the lungs, including
XX CC breast and prostate cancer. The reduction of the adenosine content of the
XX CC ONs reduces side effects. The A-containing ONs break down with the
XX CC release of deoxyadenosine which activates adenosine receptors causing
XX CC bronchoconstriction and inflammation. AAA32113 to AAA35312 represent the
XX CC nucleotide sequences given in the sequence listing from the present
XX CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
XX CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
XX CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
XX CC AAA33992) are specifically claimed ONs from the present invention. N.B.
XX CC Sequences given in the disclosure of the present invention do not match
XX CC up with their corresponding SEQ ID NO: sequences given in the sequence
XX CC listing
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGGC 8
DB 2 GCGGGGC 8
RESULT 560
AAA33230
ID AAA33230 standard; DNA; 10 BP.
XX AC AAA33230;
XX DT 28-JUL-2000 (first entry)
XX DE Low adenosine antisense oligonucleotide SEQ ID NO:919.
XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
XX KW phosphorothioate; impaired respiration; inflammation; allergy;
XX KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
XX KW antiallergic; antiasthmatic; cytotatic; analgesic; impaired airway;
XX KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
XX KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
XX KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
XX KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX OS Homo sapiens.
XX XX WO200009525-A2.
XX PN 24-FEB-2000.
XX PD 03-AUG-1999; 99WO-US017712.
XX PF

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XX PR 03-AUG-1998; 98US-0095212P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 2000-205971/18.
XX PA New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX PS Claim 18; Page 380; 1343pp; English.
XX CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers which may metastasise to the lungs, including
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 1 GGCGGGC 7

RESULT 561
AAA33200
ID AAA33200 standard; DNA; 10 BP.
AC AAA33200;
XX 28-JUL-2000 (first entry)
XX DE Low adenosine antisense oligonucleotide SEQ ID NO:889.
XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX OS Homo sapiens.

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XX PN WO200009525-A2.
XX PD 24-FEB-2000.
XX PF 03-AUG-1999; 99WO-US017712.
XX PR 03-AUG-1998; 98US-0095212P.
XX PA (UYEC-) UNIV EAST CAROLINA.
XX PI Nyce JW;
XX DR WPI; 2000-205971/18.
XX CC New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension,
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers.
XX PS Claim 18; Page 377; 1343pp; English.
XX CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impaired respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers which may metastasise to the lungs, including
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
CC nucleotide sequences given in the sequence listing from the present
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CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
CC AAA33992) are specifically claimed ONs from the present invention. N.B.
CC Sequences given in the disclosure of the present invention do not match
CC up with their corresponding SEQ ID NO: sequences given in the sequence
CC listing
XX SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGGC 8
Db 4 GGCGGGC 10

RESULT 562
AAA34000/c
ID AAA34000 standard; DNA; 10 BP.
XX AAA34000;
XX 28-JUL-2000 (first entry)
XX DT Human adenosine receptor related polynucleotide SEQ ID NO:1699.
XX DE Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW Human sapiens.

```

KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX Homo sapiens.
 OS WO200009525-A2.
 PN 24-FEB-2000.
 PD 03-AUG-1999; 99WO-US017712.
 PF 03-AUG-1998; 98US-0095212P.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA Nyce JW;
 PI WPI; 2000-205971/18.
 DR New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX Disclosure; Page 474; 1343pp; English.
 PS The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation.
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCGGGCG 9
 Db 9 GCGGGCG 3
 |||||
 |||||
 RESULT 563
 ID AAA33211 standard; DNA; 10 BP.
 XX
 AC AAA33211;
 XX
 DT 28-JUL-2000 (first entry)
 XX

DE Low adenosine antisense oligonucleotide SEQ ID NO:900.
 XX Human; adenosine receptor; low adenosine antisense oligonucleotide;
 KW phosphorothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX Homo sapiens.
 OS WO200009525-A2.
 PN 24-FEB-2000.
 PD 03-AUG-1999; 99WO-US017712.
 PF 03-AUG-1998; 98US-0095212P.
 XX (UYEC-) UNIV EAST CAROLINA.
 PA Nyce JW;
 PI WPI; 2000-205971/18.
 DR New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers.
 XX Claim 18; Page 378; 1343pp; English.
 PS The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation.
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impeded respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasise to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of the
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.
 CC Sequences given in the disclosure of the present invention do not match
 CC up with their corresponding SEQ ID NO: sequences given in the sequence
 CC listing
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGCG 8
 Db 3 GCGGGCG 9
 |||||
 |||||
 RESULT 564
 ID AAA57157

```

ID  AAA57157 standard; DNA; 10 BP.
XX
AC  AAA57157;
XX
DT  16-OCT-2000 (first entry)
XX
DE  Human intestinal trefoil factor PCR primer restriction site sequence.
XX
KW  Human intestinal trefoil factor; hITF; antiulcer; antiinflammatory;
KW  antimicrobial; cytostatic; gastrointestinal motility enhancer;
KW  peptic ulcer disease; inflammatory bowel disease; anticancer;
KW  gastrointestinal tract protection; bacterial infection; radiation injury;
KW  neoplastic cancer; ds.
XX
OS  Synthetic.
XX
XX  US6063755-A.
XX
PN  16-MAY-2000.
XX
PD
XX
PF  07-JUN-1995; 95US-00476705.
XX
XX  14-FEB-1991; 91US-00655965.
XX  13-FEB-1992; 92US-00837192.
XX  25-MAR-1993; 93US-00037741.
XX  02-FEB-1994; 94US-00191352.
XX
PA  (GENH ) GEN HOSPITAL CORP.
XX
XX  Podolsky DK;
XX
XX  WPI; 2000-364484/31.
XX
PT  New rat intestinal trefoil factor, useful for treating peptic ulcer
PT  diseases, or inflammatory bowel diseases and for protecting the
PT  intestinal tract from injury caused by bacterial infection, or radiation
PT  injury.
XX
PS  Disclosure; Col 7; 17pp; English.
XX
CC  The present sequence was added to the 5' end of primers used to amplify
CC  human intestinal trefoil factor (hITF) cDNA from a human colon cDNA
CC  library. The sequence becomes incorporated into the PCR product and, when
CC  digested, the sequence will create sticky ends to facilitate cloning of
CC  the amplified fragment. hITF may be used for the treatment of peptic
CC  ulcers and inflammatory bowel disease, and for protection of the
CC  intestinal tract from injury caused by bacterial infection or radiation
CC  injury. ITF may also be used to produce monoclonal antibodies for the
CC  detection of ITF in an intestinal tissue or blood serum by indirect
CC  immunoassay. ITF can also be used to treat neoplastic cancer
XX
SQ  Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  5 GGGCGGC 11
DB  1 GGGCGGC 7

RESULT 565
AAZ77583/c
ID  AAZ77583 standard; DNA; 10 BP.
XX
AC  AAZ77583;
XX
DT  10-APR-2000 (first entry)
XX
DE  Human dendritic cell SAGE tag, SEQ ID NO:11.
XX
KW  SAGE tag; serial analysis of gene expression; antigen-presenting cell;

```

```

KW  APC; monocyte-derived dendritic cell; differential gene expression;
KW  immunostimulatory cofactor; costimulatory factor; CTL;
XX  cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX  Homo sapiens.
XX  WO9965924-A2.
XX  23-DEC-1999.
XX  18-JUN-1999; 99WO-US013800.
XX  19-JUN-1998; 98US-0089833P.
XX  19-JUN-1998; 98US-0089844P.
XX  19-JUN-1998; 98US-0089853P.
XX  19-JUN-1998; 98US-0089878P.
XX  19-JUN-1998; 98US-0089991P.
XX  19-JUN-1998; 98US-0089992P.
XX  19-JUN-1998; 98US-0089993P.
XX  19-JUN-1998; 98US-0089994P.
XX  19-JUN-1998; 98US-0089997P.
XX  19-JUN-1998; 98US-0089999P.
XX  19-JUN-1998; 98US-0090000P.
XX  19-JUN-1998; 98US-0090035P.
XX  19-JUN-1998; 98US-0090036P.
XX  19-JUN-1998; 98US-0090039P.
XX  19-JUN-1998; 98US-0090040P.
XX  19-JUN-1998; 98US-0090041P.
XX  19-JUN-1998; 98US-0090042P.
XX  19-JUN-1998; 98US-0090043P.
XX  19-JUN-1998; 98US-0090044P.
XX  19-JUN-1998; 98US-0090045P.
XX  19-JUN-1998; 98US-0090047P.
XX  19-JUN-1998; 98US-0090048P.
XX  19-JUN-1998; 98US-0090072P.
XX  19-JUN-1998; 98US-0090076P.
XX  19-JUN-1998; 98US-0090077P.
XX  19-JUN-1998; 98US-0090078P.
XX  19-JUN-1998; 98US-0090079P.
XX  19-JUN-1998; 98US-0090080P.
XX  08-DEC-1998; 98US-0111715P.
XX  (GENZ ) GENZYME CORP.
XX  (ROBE/) ROBERTS B L.
XX  (SHAN/) SHANKARA S.
XX  Roberts BL, Shankara S;
XX  WPI; 2000-106077/09.
XX  Isolated polynucleotides differentially expressed in antigen-presenting
XX  cells, useful in gene vaccines against cancer.
XX  Claim 1; Page 63; 130pp; English.
XX  Sequences AAZ77573-779709 represent SAGE (serial analysis of gene
XX  expression) tags used to identify mRNA transcripts encoding
XX  immunostimulatory cofactor proteins which are preferentially or
XX  differentially expressed in monocyte-derived dendritic cells compared
XX  with monocytes. Some of the transcripts correspond to known genes or ESTs
XX  (expressed sequence tags) which were previously unknown to be
XX  preferentially or differentially expressed in dendritic cells, while
XX  other transcripts correspond to novel genes. Antigen-presenting cell
XX  (APC)-associated costimulatory factors play an important role in the
XX  activation of the cytotoxic immune response, particularly against tumour
XX  cells. Tumour antigen presentation via the MHC (major histocompatibility
XX  complex) and subsequent recognition by T-cell receptors is alone
XX  insufficient to activate a robust cytotoxic immune response that can lyse
XX  the tumour cells, immunostimulatory cofactors also being required for
XX  efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
XX  sequences identified using the SAGE tags have several potential uses.
XX  They may be used in vaccines to induce an immune response, particularly
XX  against a tumour antigen; to modulate the genotype of an APC; to screen

```

CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGG 7
 Db 8 CGCGGG 2

RESULT 566

AAZ78013/C
 ID AAZ78013 standard; DNA; 10 BP.

AC AAZ78013;

DT 10-APR-2000 (first entry)

DE Human dendritic cell SAGE tag, SEQ ID NO:441.

XX SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.

XX Homo sapiens.

XX WO9965924-A2.

XX 23-DEC-1999.

XX 18-JUN-1999; 99WO-US013800.

PR 19-JUN-1998; 98US-0089833P.

PR 19-JUN-1998; 98US-0089844P.

PR 19-JUN-1998; 98US-0089853P.

PR 19-JUN-1998; 98US-0089878P.

PR 19-JUN-1998; 98US-008991P.

PR 19-JUN-1998; 98US-0089992P.

PR 19-JUN-1998; 98US-0089993P.

PR 19-JUN-1998; 98US-0089994P.

PR 19-JUN-1998; 98US-0089997P.

PR 19-JUN-1998; 98US-0089999P.

PR 19-JUN-1998; 98US-0090000P.

PR 19-JUN-1998; 98US-0090035P.

PR 19-JUN-1998; 98US-0090036P.

PR 19-JUN-1998; 98US-0090039P.

PR 19-JUN-1998; 98US-0090040P.

PR 19-JUN-1998; 98US-0090042P.

PR 19-JUN-1998; 98US-0090043P.

PR 19-JUN-1998; 98US-0090044P.

PR 19-JUN-1998; 98US-0090045P.

PR 19-JUN-1998; 98US-0090047P.

PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.

PR 19-JUN-1998; 98US-0090076P.

PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.

XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.

PI Roberts BL, Shankara S;

XX MPI; 2000-106077/09.

DR Isolated polynucleotides differentially expressed in antigen-presenting
 XX cells, useful in gene vaccines against cancer.

XX Claim 1; Page 77; 130pp; English.

XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells. Immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX

SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13

Db 8 GCGGCAT 2

RESULT 567

AAZ78427/C

ID AAZ78427 standard; DNA; 10 BP.

XX AAZ78427;

XX 10-APR-2000 (first entry)

XX Human dendritic cell SAGE tag, SEQ ID NO:855.

KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 XX
 XX PD 23-DEC-1999.
 XX
 XX PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-008991P.
 PR 19-JUN-1998; 98US-008992P.
 PR 19-JUN-1998; 98US-008993P.
 PR 19-JUN-1998; 98US-008994P.
 PR 19-JUN-1998; 98US-008997P.
 PR 19-JUN-1998; 98US-008999P.
 PR 19-JUN-1998; 98US-009000P.
 PR 19-JUN-1998; 98US-009003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090075P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 DR
 XX Isolated polynucleotides differentially expressed in antigen-presenting cells, useful in gene vaccines against cancer.
 XX
 XX Claim 1; Page 90; 130pp; English.
 XX
 CC Sequences AA277573-279709 represent SAGE (serial analysis of gene expression) tags used to identify mRNA transcripts encoding immunostimulatory cofactor proteins which are preferentially or differentially expressed in monocyte-derived dendritic cells compared with monocytes. Some of the transcripts correspond to known genes or ESTs (expressed sequence tags) which were previously unknown to be preferentially or differentially expressed in dendritic cells, while other transcripts correspond to novel genes. Antigen-presenting cell (APC)-associated costimulatory factors play an important role in the activation of the cytotoxic immune response, particularly against tumour cells. Tumour antigen presentation via the MHC (major histocompatibility complex) and subsequent recognition by T-cell receptors is alone insufficient to activate a robust cytotoxic immune response that the tumour cells, immunostimulatory cofactors also being required for efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid sequences identified using the SAGE tags have several potential uses. They may be used in vaccines to induce an immune response, particularly

CC against a tumour antigen; to modulate the genotype of an APC; to screen for agents that modulate expression of differentially expressed genes in an APC; and as hybridisation probes/amplification primers for the diagnosis, prognosis and monitoring of diseases related to abnormal expression of these genes. Detection of the dendritic cell differentially expressed genes, or of their encoded proteins, can be used to identify cells as belonging to the monocyte lineage. Cells containing these genes can be used in active immunotherapy (or to stimulate production of a population of antigen-specific effector cells) and vectors containing them are used in gene therapy. Co-administration of tumour antigens and APC-associated costimulatory factors ensures adequate antigen presentation to endogenous APCs and upregulates the APCs for the presentation of co-stimulatory signals, migration to T cell-rich sites, secretion of T cell growth factors and secretion of chemokines for recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred.No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCGGC 11
 Db 10 GGGCGGC 4
 RESULT 568
 AAZ79040
 ID AAZ79040 standard; DNA; 10 BP.
 XX AC AAZ79040;
 XX DT 10-APR-2000 (first entry)
 XX Human dendritic cell SAGE tag, SEQ ID NO:1468.
 DE SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 XX PD 23-DEC-1999.
 XX PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-008991P.
 PR 19-JUN-1998; 98US-008992P.
 PR 19-JUN-1998; 98US-008993P.
 PR 19-JUN-1998; 98US-008994P.
 PR 19-JUN-1998; 98US-008997P.
 PR 19-JUN-1998; 98US-008999P.
 PR 19-JUN-1998; 98US-009000P.
 PR 19-JUN-1998; 98US-009003P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.
 PR 19-JUN-1998; 98US-0090072P.

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PR 19-JUN-1998; 98US-0090076P.
PR 19-JUN-1998; 98US-0090077P.
PR 19-JUN-1998; 98US-0090078P.
PR 19-JUN-1998; 98US-0090079P.
PR 19-JUN-1998; 98US-0090080P.
PR 08-DEC-1998; 98US-0111715P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
DR
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
PT
XX
XX Claim 1; Page 107; 130pp; English.
PS
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.
CC They may be used in vaccines to induce an immune response, particularly
CC against a tumour antigen; to modulate the genotype of an APC; to screen
CC for agents that modulate expression of differentially expressed genes in
CC an APC; and as hybridisation probes/amplification primers for the
CC diagnosis, prognosis and monitoring of diseases related to abnormal
CC expression of these genes. Detection of the dendritic cell differentially
CC expressed genes, or of their encoded proteins, can be used to identify
CC cells as belonging to the monocyte lineage. Cells containing these genes
CC can be used in active immunotherapy (or to stimulate production of a
CC population of antigen-specific effector cells) and vectors containing and
CC them are used in gene therapy. Co-administration of tumour antigens and
CC APC-associated costimulatory factors ensures adequate antigen
CC presentation to endogenous APCs and upregulates the APCs for the
CC presentation of co-stimulatory signals, migration to T cell-rich sites,
CC secretion of T cell growth factors and secretion of chemokines for
CC recruitment of immune effector cells
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

```

```

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GCGGGCG 9
Db 3 GCGGGCG 9

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RESULT 569
AAZ79696/c
ID AAZ79696 standard; DNA; 10 BP.
XX
AC AAZ79696;
XX

```

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DT 10-APR-2000 (first entry)
XX

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DE Human dendritic cell SAGE tag, SEQ ID NO:2124.

```

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XX
KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
KW APC; monocyte-derived dendritic cell; differential gene expression;
KW immunostimulatory cofactor; costimulatory factor; CTL;
KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
XX
OS Homo sapiens.
XX
XX WO965924-A2.
XX
XX 23-DEC-1999.
XX
XX 18-JUN-1999; 99WO-US013800.
XX
XX 19-JUN-1998; 98US-0089833P.
XX 19-JUN-1998; 98US-0089844P.
XX 19-JUN-1998; 98US-0089853P.
XX 19-JUN-1998; 98US-0089878P.
XX 19-JUN-1998; 98US-0089911P.
XX 19-JUN-1998; 98US-0089922P.
XX 19-JUN-1998; 98US-0089933P.
XX 19-JUN-1998; 98US-0089997P.
XX 19-JUN-1998; 98US-0089999P.
XX 19-JUN-1998; 98US-0090000P.
XX 19-JUN-1998; 98US-0090035P.
XX 19-JUN-1998; 98US-0090036P.
XX 19-JUN-1998; 98US-0090039P.
XX 19-JUN-1998; 98US-0090040P.
XX 19-JUN-1998; 98US-0090041P.
XX 19-JUN-1998; 98US-0090042P.
XX 19-JUN-1998; 98US-0090043P.
XX 19-JUN-1998; 98US-0090044P.
XX 19-JUN-1998; 98US-0090045P.
XX 19-JUN-1998; 98US-0090047P.
XX 19-JUN-1998; 98US-0090048P.
XX 19-JUN-1998; 98US-0090072P.
XX 19-JUN-1998; 98US-0090076P.
XX 19-JUN-1998; 98US-0090077P.
XX 19-JUN-1998; 98US-0090078P.
XX 19-JUN-1998; 98US-0090079P.
XX 19-JUN-1998; 98US-0090080P.
XX 08-DEC-1998; 98US-0111715P.
XX
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
XX
XX WPI; 2000-106077/09.
XX
XX Isolated polynucleotides differentially expressed in antigen-presenting
PT cells, useful in gene vaccines against cancer.
PT
XX
XX Claim 1; Page 125; 130pp; English.
XX
XX Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
CC expression) tags used to identify mRNA transcripts encoding
CC immunostimulatory cofactor proteins which are preferentially or
CC differentially expressed in monocyte-derived dendritic cells compared
CC with monocytes. Some of the transcripts correspond to known genes or ESTs
CC (expressed sequence tags) which were previously unknown to be
CC preferentially or differentially expressed in dendritic cells, while
CC other transcripts correspond to novel genes. Antigen-presenting cell
CC (APC)-associated costimulatory factors play an important role in the
CC activation of the cytotoxic immune response, particularly against tumour
CC cells. Tumour antigen presentation via the MHC (major histocompatibility
CC complex) and subsequent recognition by T-cell receptors is alone
CC insufficient to activate a robust cytotoxic immune response that can lyse
CC the tumour cells, immunostimulatory cofactors also being required for
CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
CC sequences identified using the SAGE tags have several potential uses.

```

CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 6 C; 3 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGGG 7
 Db 8 CGCGGG 2
 RESULT 570
 AAZ79088/c
 ID AAZ79088 standard; DNA; 10 BP.
 XX
 AC AAZ79088;
 XX
 DT 10-APR-2000 (first entry)
 XX
 DE Human dendritic cell SAGE tag, SEQ ID NO:1516.
 XX
 KW SAGE tag; serial analysis of gene expression; antigen-presenting cell;
 KW APC; monocyte-derived dendritic cell; differential gene expression;
 KW immunostimulatory cofactor; costimulatory factor; CTL;
 KW cytotoxic T-lymphocyte; tumour antigen; immunotherapy; anticancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO9965924-A2.
 PN
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013800.
 XX
 PR 19-JUN-1998; 98US-0089833P.
 PR 19-JUN-1998; 98US-0089844P.
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089878P.
 PR 19-JUN-1998; 98US-0089991P.
 PR 19-JUN-1998; 98US-0089992P.
 PR 19-JUN-1998; 98US-0089993P.
 PR 19-JUN-1998; 98US-0089994P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0089999P.
 PR 19-JUN-1998; 98US-0090000P.
 PR 19-JUN-1998; 98US-0090035P.
 PR 19-JUN-1998; 98US-0090036P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 PR 19-JUN-1998; 98US-0090042P.
 PR 19-JUN-1998; 98US-0090043P.
 PR 19-JUN-1998; 98US-0090044P.
 PR 19-JUN-1998; 98US-0090045P.
 PR 19-JUN-1998; 98US-0090047P.
 PR 19-JUN-1998; 98US-0090048P.

PR 19-JUN-1998; 98US-0090072P.
 PR 19-JUN-1998; 98US-0090076P.
 PR 19-JUN-1998; 98US-0090077P.
 PR 19-JUN-1998; 98US-0090078P.
 PR 19-JUN-1998; 98US-0090079P.
 PR 19-JUN-1998; 98US-0090080P.
 PR 08-DEC-1998; 98US-0111715P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 XX WPI; 2000-106077/09.
 XX
 PT Isolated polynucleotides differentially expressed in antigen-presenting
 PT cells, useful in gene vaccines against cancer.
 XX
 PS Claim 1; Page 108; 130pp; English.
 XX
 CC Sequences AAZ77573-279709 represent SAGE (serial analysis of gene
 CC expression) tags used to identify mRNA transcripts encoding
 CC immunostimulatory cofactor proteins which are preferentially or
 CC differentially expressed in monocyte-derived dendritic cells compared
 CC with monocytes. Some of the transcripts correspond to known genes or ESTs
 CC (expressed sequence tags) which were previously unknown to be
 CC preferentially or differentially expressed in dendritic cells, while
 CC other transcripts correspond to novel genes. Antigen-presenting cell
 CC (APC)-associated costimulatory factors play an important role in the
 CC activation of the cytotoxic immune response, particularly against tumour
 CC cells. Tumour antigen presentation via the MHC (major histocompatibility
 CC complex) and subsequent recognition by T-cell receptors is alone
 CC insufficient to activate a robust cytotoxic immune response that can lyse
 CC the tumour cells, immunostimulatory cofactors also being required for
 CC efficient activation of cytotoxic T-lymphocytes (CTLs). Nucleic acid
 CC sequences identified using the SAGE tags have several potential uses.
 CC They may be used in vaccines to induce an immune response, particularly
 CC against a tumour antigen; to modulate the genotype of an APC; to screen
 CC for agents that modulate expression of differentially expressed genes in
 CC an APC; and as hybridisation probes/amplification primers for the
 CC diagnosis, prognosis and monitoring of diseases related to abnormal
 CC expression of these genes. Detection of the dendritic cell differentially
 CC expressed genes, or of their encoded proteins, can be used to identify
 CC cells as belonging to the monocyte lineage. Cells containing these genes
 CC can be used in active immunotherapy (or to stimulate production of a
 CC population of antigen-specific effector cells) and vectors containing
 CC them are used in gene therapy. Co-administration of tumour antigens and
 CC APC-associated costimulatory factors ensures adequate antigen
 CC presentation to endogenous APCs and upregulates the APCs for the
 CC presentation of co-stimulatory signals, migration to T cell-rich sites,
 CC secretion of T cell growth factors and secretion of chemokines for
 CC recruitment of immune effector cells
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GCGCGCA 12
 Db 8 GCGCGCA 2
 RESULT 571
 AAZ85222
 ID AAZ85222 standard; DNA; 10 BP.
 XX
 AC AAZ85222;
 XX
 DT 07-APR-2000 (first entry)
 XX

DE Metastatic breast tumour cell downregulated transcript tag #4456.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 OS Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.
 XX 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 178; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCGGGCG 9
 Db 1 GCGGGCG 7
 |||||
 RESULT 572
 AAZ85111/c
 ID AAZ85111 standard; DNA; 10 BP.
 XX AAZ85111;
 AC AAZ85111;
 XX

DT 07-APR-2000 (first entry)
 XX Metastatic breast tumour cell downregulated transcript tag #4345.
 XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX Homo sapiens.
 XX WO9965928-A2.
 XX 23-DEC-1999.
 XX 18-JUN-1999; 99WO-US013647.
 XX 19-JUN-1998; 98US-0089853P.
 XX 19-JUN-1998; 98US-0089997P.
 XX 19-JUN-1998; 98US-0090039P.
 XX 19-JUN-1998; 98US-0090040P.
 XX 19-JUN-1998; 98US-0090041P.
 XX (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX Roberts BL, Shankara S;
 PI WPI; 2000-106079/09.
 XX Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX Claim 1; Page 175; 219pp; English.
 XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in
 CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGCG 8
 Db 7 GCGGGCG 1
 |||||
 RESULT 573
 AAZ81013/c
 ID AAZ81013 standard; DNA; 10 BP.
 XX

```

AC AAZ81013;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #247.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 64; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCGC 11
|||||
DB 10 GCGCGC 4

RESULT 574
AAZ82036

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```

ID AAZ82036 standard; DNA; 10 BP.
XX
AC AAZ82036;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1270.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
DR WPI; 2000-106079/09.
XX
PT Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 92; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
|||||
DB 3 GCGCGCA 9

```

RESULT 575
AAZ82118
ID AAZ82118 standard; DNA; 10 BP.
XX
XX AAZ82118;
AC
XX 07-APR-2000 (first entry)
DT
XX Metastatic breast tumour cell upregulated transcript tag #1352.
DE
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
XX Homo sapiens.
OS
XX WO9965928-A2.
PN
XX 23-DEC-1999.
PD
XX
PF 18-JUN-1999; 99WO-US013647.
XX
XX 19-JUN-1998; 98US-0089853P.
PR
XX 19-JUN-1998; 98US-0089997P.
PR
XX 19-JUN-1998; 98US-0090039P.
PR
XX 19-JUN-1998; 98US-0090040P.
PR
XX 19-JUN-1998; 98US-0090041P.
XX
XX (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
XX Roberts BL, Shankara S;
PI
XX WPI; 2000-106079/09.
PI
XX
DR
XX Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
XX Claim 1; Page 95; 219pp; English.
XX
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic. Diagnosis is
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC vaccines; for diagnosing breast cancer and for raising specific
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
XX Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCGGGCG 9
DB |||||
4 GCGGGCG 10

Db	3	GGGGGG	9	Qy	6	GGGGCA	12
				Db	9	GGGGCA	3
RESULT 577							
AAZ81107/c							
ID	AAZ81107	standard; DNA; 10 BP.					
XX	AC	AAZ81107;					
XX	DT	07-APR-2000 (first entry)					
XX	DE	Metastatic breast tumour cell upregulated transcript tag #341.					
XX	DE	Human; metastatic breast tumour tissue; breast cancer; tag; primer;					
KW	KW	non-metastatic breast tumour tissue; gene therapy; anticancer;					
KW	KW	antimetastatic; vaccine; diagnosis; ss.					
XX	OS	Homo sapiens.					
XX	OS	WO9965928-A2.					
PN	PN	23-DEC-1999.					
XX	XX	18-JUN-1999; 99WO-US013647.					
XX	PF	19-JUN-1998; 98US-0089853P.					
PR	PR	19-JUN-1998; 98US-0089997P.					
PR	PR	19-JUN-1998; 98US-0090039P.					
PR	PR	19-JUN-1998; 98US-0090040P.					
PR	PR	19-JUN-1998; 98US-0090041P.					
XX	XX	(GENZ) GENZYME CORP.					
PA	PA	(ROBE/) ROBERTS B L.					
PA	PA	(SHAN/) SHANKARA S.					
XX	XX	Roberts BL, Shankara S;					
XX	PI	WPI; 2000-106079/09.					
XX	DR	WPI; 2000-106079/09.					
XX	XX	Isolated polynucleotides differentially expressed between metastatic and					
PT	PT	non-metastatic breast cancer cells, useful for diagnosis, prevention and					
PT	PT	treatment of cancer.					
XX	PS	Claim 1; Page 67; 219pp; English.					
XX	XX	AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts					
CC	CC	that are preferentially transcribed in the metastatic breast tumour					
CC	CC	tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942					
CC	CC	to AAZ86677 represent tags corresponding to distinct transcripts that are					
CC	CC	preferentially transcribed in the primary or non-metastatic breast tumour					
CC	CC	tissue (i.e. are downregulated in metastatic breast tumour cells). These					
CC	CC	transcripts can be used for diagnosis, prognosis, monitoring and					
CC	CC	treatment of breast cancer, particularly where metastatic. Diagnosis is					
CC	CC	by standard immunoassays or hybridisation/amplification reactions.					
CC	CC	Compounds that modulate expression of the transcripts are potentially					
CC	CC	useful for treatment of (metastatic) breast cancer, while promoters from					
CC	CC	the transcripts are used to direct expression, in selected cell types, of					
CC	CC	e.g. therapeutic genes (also ribozymes or antisense sequences),					
CC	CC	particularly an antigen-encoding sequence for use in gene or cell-based					
CC	CC	vaccines. Polypeptides encoded by the transcripts are also useful in					
CC	CC	vaccines; for diagnosing breast cancer and for raising specific					
CC	CC	antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic					
CC	CC	agents. Host cells that produce the polypeptides can be used to expand					
CC	CC	and isolate populations of educated, antigen-specific immune effector					
CC	CC	cells, e.g. cytotoxic T lymphocytes, and these used for adoptive					
CC	CC	immunotherapy					
XX	XX	Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;					
SQ	SQ	Sequence 10 BP; 0 A; 5 C; 3 G; 0 T; 0 U; 0 Other;					
		Query Match 43.8%; Score 7; DB 1; Length 10;					
		Best Local Similarity 100.0%; Pred. No. 3.4e+02;					
		Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Gaps 0; Indels 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 9 GGGCGGC 3

RESULT 579
AAZ83948/c
ID AAZ83948 standard; DNA; 10 BP.
AC AAZ83948;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell downregulated transcript tag #3182.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN W09965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 144; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic.
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX
SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGG 7
| | | | |
Db 8 CGCGCGG 2

RESULT 580
AAZ82637/c
ID AAZ82637 standard; DNA; 10 BP.
XX
AC AAZ82637;
XX
DT 07-APR-2000 (first entry)
XX
DE Metastatic breast tumour cell upregulated transcript tag #1871.
XX
KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX
OS Homo sapiens.
XX
PN W09965928-A2.
XX
PD 23-DEC-1999.
XX
PF 18-JUN-1999; 99WO-US013647.
XX
PR 19-JUN-1998; 98US-0089853P.
PR 19-JUN-1998; 98US-0089997P.
PR 19-JUN-1998; 98US-0090039P.
PR 19-JUN-1998; 98US-0090040P.
PR 19-JUN-1998; 98US-0090041P.
XX
PA (GENZ) GENZYME CORP.
PA (ROBE/) ROBERTS B L.
PA (SHAN/) SHANKARA S.
XX
PI Roberts BL, Shankara S;
XX
XX WPI; 2000-106079/09.
XX
DR Isolated polynucleotides differentially expressed between metastatic and
PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
PT treatment of cancer.
XX
PS Claim 1; Page 109; 219pp; English.
XX
CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
CC that are preferentially transcribed in the metastatic breast tumour
CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
CC to AAZ86677 represent tags corresponding to distinct transcripts that are
CC preferentially transcribed in the primary or non-metastatic breast tumour
CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
CC transcripts can be used for diagnosis, prognosis, monitoring and
CC treatment of breast cancer, particularly where metastatic.
CC by standard immunoassays or hybridisation/amplification reactions.
CC Compounds that modulate expression of the transcripts are potentially
CC useful for treatment of (metastatic) breast cancer, while promoters from
CC the transcripts are used to direct expression, in selected cell types, of
CC e.g. therapeutic genes (also ribozymes or antisense sequences),
CC particularly an antigen-encoding sequence for use in gene or cell-based
CC vaccines. Polypeptides encoded by the transcripts are also useful in
CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
CC agents. Host cells that produce the polypeptides can be used to expand
CC and isolate populations of educated, antigen-specific immune effector
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX

```
XX SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GGGCGGC 11
Db 7 GGGCGGC 1
RESULT 581
AAZ84974/C
ID AAZ84974 standard; DNA; 10 BP.
XX AC AAZ84974;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #4208.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 171; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
```

```
CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
CC immunotherapy
XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 CGGCATC 14
Db 10 CGGCATC 4
RESULT 582
AAZ85908
ID AAZ85908 standard; DNA; 10 BP.
XX AC AAZ85908;
XX DT 07-APR-2000 (first entry)
XX DE Metastatic breast tumour cell downregulated transcript tag #5142.
XX Human; metastatic breast tumour tissue; breast cancer; tag; primer;
KW non-metastatic breast tumour tissue; gene therapy; anticancer;
KW antimetastatic; vaccine; diagnosis; ss.
XX OS Homo sapiens.
XX WO9965928-A2.
XX PD 23-DEC-1999.
XX PF 18-JUN-1999; 99WO-US013647.
XX PR 19-JUN-1998; 98US-0089853P.
XX PR 19-JUN-1998; 98US-0089997P.
XX PR 19-JUN-1998; 98US-0090039P.
XX PR 19-JUN-1998; 98US-0090040P.
XX PR 19-JUN-1998; 98US-0090041P.
XX (GENZ ) GENZYME CORP.
XX (ROBE/) ROBERTS B L.
XX (SHAN/) SHANKARA S.
XX PI Roberts BL, Shankara S;
XX WPI; 2000-106079/09.
XX Isolated polynucleotides differentially expressed between metastatic and
XX non-metastatic breast cancer cells, useful for diagnosis, prevention and
XX treatment of cancer.
XX Claim 1; Page 195; 219pp; English.
XX AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
XX that are preferentially transcribed in the metastatic breast tumour
XX tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
XX to AAZ86677 represent tags corresponding to distinct transcripts that are
XX preferentially transcribed in the primary or non-metastatic breast tumour
XX tissue (i.e. are downregulated in metastatic breast tumour cells). These
XX transcripts can be used for diagnosis, prognosis, monitoring and
XX treatment of breast cancer, particularly where metastatic. Diagnosis is
XX by standard immunoassays or hybridisation/amplification reactions.
XX Compounds that modulate expression of the transcripts are potentially
XX useful for treatment of (metastatic) breast cancer, while promoters from
XX the transcripts are used to direct expression, in selected cell types, of
XX e.g. therapeutic genes (also ribozymes or antisense sequences),
XX particularly an antigen-encoding sequence for use in gene or cell-based
XX vaccines. Polypeptides encoded by the transcripts are also useful in
XX vaccines; for diagnosing breast cancer and for raising specific
XX antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
XX agents. Host cells that produce the polypeptides can be used to expand
XX and isolate populations of educated, antigen-specific immune effector
```

CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 7 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGC 8
 Db 4 GCGGGC 10
 RESULT 583
 AAZ86394
 ID AAZ86394 standard; DNA; 10 BP.
 XX
 AC AAZ86394;
 XX
 DT 07-APR-2000 (first entry)
 XX
 DE Metastatic breast tumour cell downregulated transcript tag #5628.
 XX
 KW Human; metastatic breast tumour tissue; breast cancer; tag; primer;
 KW non-metastatic breast tumour tissue; gene therapy; anticancer;
 KW antimetastatic; vaccine; diagnosis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO9965928-A2.
 XX
 PD 23-DEC-1999.
 XX
 PF 18-JUN-1999; 99WO-US013647.
 XX
 PR 19-JUN-1998; 98US-0089853P.
 PR 19-JUN-1998; 98US-0089997P.
 PR 19-JUN-1998; 98US-0090039P.
 PR 19-JUN-1998; 98US-0090040P.
 PR 19-JUN-1998; 98US-0090041P.
 XX
 PA (GENZ) GENZYME CORP.
 PA (ROBE/) ROBERTS B L.
 PA (SHAN/) SHANKARA S.
 XX
 PI Roberts BL, Shankara S;
 XX
 PS WPI; 2000-106079/09.
 XX
 DR Isolated polynucleotides differentially expressed between metastatic and
 PT non-metastatic breast cancer cells, useful for diagnosis, prevention and
 PT treatment of cancer.
 XX
 PS Claim 1; Page 207; 219pp; English.
 XX
 CC AAZ80767 to AAZ83941 represent tags corresponding to distinct transcripts
 CC that are preferentially transcribed in the metastatic breast tumour
 CC tissue (i.e. are upregulated in metastatic breast tumour cells). AAZ83942
 CC to AAZ86677 represent tags corresponding to distinct transcripts that are
 CC preferentially transcribed in the primary or non-metastatic breast tumour
 CC tissue (i.e. are downregulated in metastatic breast tumour cells). These
 CC transcripts can be used for diagnosis, prognosis, monitoring and
 CC treatment of breast cancer, particularly where metastatic. Diagnosis is
 CC by standard immunoassays or hybridisation/amplification reactions.
 CC Compounds that modulate expression of the transcripts are potentially
 CC useful for treatment of (metastatic) breast cancer, while promoters from
 CC the transcripts are used to direct expression, in selected cell types, of
 CC e.g. therapeutic genes (also ribozymes or antisense sequences),
 CC particularly an antigen-encoding sequence for use in gene or cell-based
 CC vaccines. Polypeptides encoded by the transcripts are also useful in

CC vaccines; for diagnosing breast cancer and for raising specific
 CC antibodies (Ab). Ab are used to detect the polypeptides or as therapeutic
 CC agents. Host cells that produce the polypeptides can be used to expand
 CC and isolate populations of educated, antigen-specific immune effector
 CC cells, e.g. cytotoxic T lymphocytes, and these used for adoptive
 CC immunotherapy
 XX
 SQ Sequence 10 BP; 3 A; 2 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GCGGGCA 12
 Db 2 GCGGGCA 8
 RESULT 584
 AAA93863/c
 ID AAA93863 standard; DNA; 10 BP.
 XX
 AC AAA93863;
 XX
 DT 11-JAN-2001 (first entry)
 XX
 DE Oligonucleotide used in computational methodology SEQ ID 31.
 XX
 KW Biopolymer; sequence cluster; sequence analysis; ss.
 XX
 OS Synthetic.
 XX
 PN US6109776-A.
 XX
 PD 29-AUG-2000.
 XX
 PF 21-APR-1998; 98US-00063450.
 XX
 PR 21-APR-1998; 98US-00063450.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Haas J;
 XX
 DR WPI; 2000-586307/55.
 XX
 PT Computational method and system for identifying clusters of sequences
 PT within a set of sequences, useful for identifying, e.g. DNA-binding
 PT sites.
 XX
 PS Disclosure; Col 35; 38pp; English.
 XX
 CC A computational analysis method can be used to identify new biopolymer
 CC sequence clusters from sequence sets. The method comprises placing each
 CC sequence into a new cluster, and calculating an initial information
 CC weight matrix. Other sequences from the set are added to the cluster and
 CC the information weight matrix of the cluster is re-computed until the
 CC information content of the matrix falls below a threshold. The method is
 CC useful for identifying potential DNA-binding sites from a set of
 CC oligonucleotide sequences. The method and system may also be used to
 CC analyse different types of sequences, e.g. the sequences of amino acid
 CC subunits in protein polymers may be analysed to identify common or
 CC conserved amino acid subunit sub-sequences within the polymers that
 CC correspond to common structural features within a family of proteins. The
 CC present sequence represents a synthetic oligonucleotide used to
 CC illustrate the method of the invention
 XX
 SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Genes most frequently expressed in human monocytes and GM-macrophages and
 PT M-macrophages studied and with cDNAs characterized, for study of gene
 PT specificity, disease onset mechanism, drug development and diagnosis.
 XX
 XX Claim 43; Page 128; 138pp; Japanese.

CC The present invention describes 100 human genes, which are expressed most
 CC frequently in human monocytes. The cDNA of each gene has a sequence fully
 CC defined in the specification, and lacking the CATG sequence located
 CC adjacent to polyA region. Also described are: (1) an antibody
 CC specifically for the protein encoded by any of the genes; (2)
 CC oligonucleotides obtained from the cDNA sequences; (3) 380 human genes
 CC which are expressed most frequently in human macrophages, differentiated
 CC from human monocytes by granulocyte-macrophage colony-stimulating factor,
 CC the cDNA of each gene has a fully defined sequence, given in the
 CC specification, lacking the base sequence CATG located most closely to the
 CC poly A region; (4) an antibody specifically for the protein encoded by
 CC any of the genes of (3); and (5) oligonucleotides obtained from the cDNA
 CC sequences of (3). The genes and cDNAs, are used for the study of gene
 CC specificity and disease onset mechanism e.g. oncogenesis, genetic
 CC diseases, drug development and diagnosis. AAA56107 to AAA56586 represent
 CC specifically claimed oligonucleotide tag sequences for human genes
 CC expressed in monocytes and macrophages

SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9

DB 3 GCGGGCG 9

RESULT 588

AAA03580

ID AAA03580 standard; DNA; 10 BP.

AC AAA03580;

DT 19-MAY-2000 (first entry)

DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:864.

XX Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
 KW adenosine A2a receptor; adenosine A3 receptor; adenosine A3 receptor;
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
 KW endotoxin release; ARDS; acute respiratory distress syndrome;
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
 KW chronic obstructive pulmonary disease; ss.

OS Homo sapiens.

OS Synthetic.

PN WO9963938-A2.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012775.

XX 08-JUN-1998; 98US-0088501P.

PR 09-JUN-1998; 98US-00093972.

PR 09-JUN-1998; 98US-0088657P.

XX (EPIC-) EPIGENESIS PHARM INC.

XX Nyce JW, Hill JL;

XX WPI; 2000-116433/10.

PT Novel composition for treating or preventing e.g. cardiopulmonary and
 PT renal injury.

PS Claim 17; Page 36; 252pp; English.

XX The present invention describes a pharmaceutical composition, comprising
 CC at least one agent (I) that prevents, alleviates and/or inhibits
 CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
 CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
 CC (Ib), containing less than 15% adenosine (A), that is antisense to target
 CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3'
 CC ends or segments between coding and non-coding sequences), or to all
 CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
 CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
 CC and (Ib), and optionally also contains one or more surfactants. The
 CC compositions are used to prevent, alleviate and/or treat adenosine
 CC receptor-mediated cardiac, lung and/or renal damage or failure
 CC (particularly where associated with ischaemia, toxin release and/or
 CC administration of drugs or imaging agents, e.g. adenosine for treating
 CC supraventricular tachycardia); (adult) respiratory distress syndrome
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration
 CC of stress-test agents, particularly where such conditions are associated
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
 CC AAA03715 represent specifically claimed phosphorothioate antisense
 CC oligonucleotides for use in the composition of the present invention.
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
 CC phosphorothioate oligonucleotides used in the exemplification of the
 CC present invention

XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGCG 8

DB 2 GCGGGCG 8

RESULT 589

AAA03589

ID AAA03589 standard; DNA; 10 BP.

AC AAA03589;

DT 19-MAY-2000 (first entry)

DE Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:873.

XX Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
 KW adenosine A2a receptor; adenosine A3 receptor; adenosine A3 receptor;
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
 KW endotoxin release; ARDS; acute respiratory distress syndrome;
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
 KW chronic obstructive pulmonary disease; ss.

OS Homo sapiens.

OS Synthetic.

PN WO9963938-A2.

XX 16-DEC-1999.

XX 08-JUN-1999; 99WO-US012775.

XX 08-JUN-1998; 98US-0088501P.

PR 09-JUN-1998; 98US-00093972.

PR 09-JUN-1998; 98US-0088657P.

PA (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Hill JL;
 PI WPI; 2000-116433/10.
 XX Novel composition for treating or preventing e.g. cardiopulmonary and
 PT renal injury.
 PT Claim 17; Page 36; 252pp; English.
 XX The present invention describes a pharmaceutical composition, comprising
 XX at least one agent (I) that prevents, alleviates and/or inhibits
 CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
 CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
 CC (Ib), containing less than 15% adenosine (A), that is antisense to target
 CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
 CC ends or segments between coding and non-coding sequences), or to all
 CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
 CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
 CC and (Ib), and optionally also contains one or more surfactants. The
 CC compositions are used to prevent, alleviate and/or treat adenosine
 CC receptor-mediated cardiac, lung and/or renal damage or failure
 CC (particularly where associated with ischaemia, toxin release and/or
 CC administration of drugs or imaging agents, e.g. adenosine for treating
 CC supraventricular tachycardia); (adult) respiratory distress syndrome
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration
 CC of stress-test agents, particularly where such conditions are associated
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
 CC AAA03715 represent specifically claimed phosphorothioate antisense
 CC oligonucleotides for use in the composition of the present invention.
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
 CC phosphorothioate oligonucleotides used in the exemplification of the
 CC present invention
 XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGC 8
 DB 1 GCGGGC 7
 XX
 AC AAA03559;
 XX 19-MAY-2000 (first entry)
 XX Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:843.
 DE Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
 KW adenosine A2a receptor; adenosine A2b receptor; adenosine A3 receptor;
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
 KW endotoxin release; ARDS; acute respiratory distress syndrome;
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
 KW chronic obstructive pulmonary disease; ss.
 XX Homo sapiens.
 OS Synthetic.
 XX WO9963938-A2.
 PN 16-DEC-1999.
 PD
 XX

PF 08-JUN-1999; 99WO-US012775.
 XX 08-JUN-1998; 98US-0088501P.
 PR 09-JUN-1998; 98US-00093972.
 PR 09-JUN-1998; 98US-0088657P.
 XX (EPIG-) EPIGENESIS PHARM INC.
 XX Nyce JW, Hill JL;
 PI WPI; 2000-116433/10.
 XX Novel composition for treating or preventing e.g. cardiopulmonary and
 PT renal injury.
 PT Claim 17; Page 36; 252pp; English.
 XX The present invention describes a pharmaceutical composition, comprising
 XX at least one agent (I) that prevents, alleviates and/or inhibits
 CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
 CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
 CC (Ib), containing less than 15% adenosine (A), that is antisense to target
 CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
 CC ends or segments between coding and non-coding sequences), or to all
 CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
 CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
 CC and (Ib), and optionally also contains one or more surfactants. The
 CC compositions are used to prevent, alleviate and/or treat adenosine
 CC receptor-mediated cardiac, lung and/or renal damage or failure
 CC (particularly where associated with ischaemia, toxin release and/or
 CC administration of drugs or imaging agents, e.g. adenosine for treating
 CC supraventricular tachycardia); (adult) respiratory distress syndrome
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration
 CC of stress-test agents, particularly where such conditions are associated
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
 CC AAA03715 represent specifically claimed phosphorothioate antisense
 CC oligonucleotides for use in the composition of the present invention.
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
 CC phosphorothioate oligonucleotides used in the exemplification of the
 CC present invention
 XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGC 8
 DB 4 GCGGGC 10
 XX
 AC AAA03570;
 XX 19-MAY-2000 (first entry)
 XX Human adenosine A1 receptor antisense oligonucleotide SEQ ID NO:854.
 DE Human; adenosine A1 receptor; antisense oligonucleotide; hypoxia;
 KW adenosine A2a receptor; adenosine A2b receptor; adenosine A3 receptor;
 KW phosphorothioate; cardiopulmonary failure; renal failure; ischaemia;
 KW endotoxin release; ARDS; acute respiratory distress syndrome;
 KW cytoprotective; anti-allergic; anti-inflammatory; anti-hypoxic;
 KW supraventricular tachycardia; allergic rhinitis; acute inflammation;
 KW chronic obstructive pulmonary disease; ss.
 XX Homo sapiens.
 OS

OS Synthetic.
 XX W09963938-A2.
 XX
 PD 16-DEC-1999.
 XX
 XX 08-JUN-1999; 99WO-US012775.
 XX
 XX 08-JUN-1998; 98US-0088501P.
 PR 09-JUN-1998; 98US-00093972.
 PR 09-JUN-1998; 98US-0088657P.
 XX
 PA (EPIC-) EPIGENESIS PHARM INC.
 XX
 PI Nyce JW, Hill JL;
 XX
 XX WPI; 2000-116433/10.
 DR
 XX Novel composition for treating or preventing e.g. cardiopulmonary and
 PT renal injury.
 PT
 XX
 PS Claim 17; Page 36; 252pp; English.
 XX
 CC The present invention describes a pharmaceutical composition, comprising
 CC at least one agent (I) that prevents, alleviates and/or inhibits
 CC adenosine-mediated cardiopulmonary and/or renal damage and/or failure.
 CC (I) is an adenosine A2a receptor agonist (Ia), or an oligonucleotide
 CC (Ib), containing less than 15% adenosine (A), that is antisense to target
 CC genes or corresponding RNA, to genomic flanking regions (i.e. 5' or 3',
 CC ends or segments between coding and non-coding sequences), or to all
 CC segments of mRNA encoding the adenosine A1, A2a, A2b or A3 receptors, and
 CC has A1, A2b or A3 agonist activity or A2a antagonist activity (or at
 CC least no agonist activity at this receptor). (I) may be a mixture of (Ia)
 CC and (Ib), and optionally also contains one or more surfactants. The
 CC compositions are used to prevent, alleviate and/or treat adenosine
 CC receptor-mediated cardiac, lung and/or renal damage or failure
 CC (particularly where associated with ischaemia, toxin release and/or
 CC administration of drugs or imaging agents, e.g. adenosine for treating
 CC supraventricular tachycardia); (adult) respiratory distress syndrome
 CC (e.g. associated with sepsis); allergic rhinitis; chronic obstructive
 CC pulmonary disease; cardiopulmonary hypoxia associated with administration
 CC of stress-test agents, particularly where such conditions are associated
 CC with acute inflammation. AAA02717, AAA02719, AAA02721 and AAA02723 to
 CC AAA03715 represent specifically claimed phosphorothioate antisense
 CC oligonucleotides for use in the composition of the present invention.
 CC AAA02718, AAA02720, AAA02722 and AAA03716 to AAA03720 represent other
 CC phosphorothioate oligonucleotides used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGGC 8
 Db 3 GCGGGGC 9
 |||||
 |||||
 RESULT 592
 AAF19333
 ID AAF19333 standard; DNA; 10 BP.
 AC
 AC AAF19333;
 XX
 XX 14-MAR-2001 (first entry)
 DT
 XX Human adenosine A1 receptor polynucleotide fragment #900.
 DE
 XX
 XX Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiaesthetic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX Homo sapiens.
 OS
 XX W0200062736-A2.
 PN
 XX 26-OCT-2000.
 PD
 XX 24-MAR-2000; 2000WO-US008020.
 PF
 XX 06-APR-1999; 99US-0127958P.
 PR
 XX (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 XX Nyce JW;
 PI
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 120; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiaesthetic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
 Db 3 GCGGGGC 9
 |||||
 |||||

RESULT 593

AAAF19343
 ID AAAF19343 standard; DNA; 10 BP.
 XX
 AC AAAF19343;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human adenosine A1 receptor polynucleotide fragment #910.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 120; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAAF19343 to AAAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGC 8
 Db 2 GCGGGC 8
 RESULT 594
 AAAF19352
 ID AAAF19352 standard; DNA; 10 BP.
 XX
 AC AAAF19352;
 XX
 DT 14-MAR-2001 (first entry)
 XX
 DE Human adenosine A1 receptor polynucleotide fragment #919.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 DR
 XX Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 120; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAAF19343 to AAAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX

CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGGGGC 8
 Db 1 GCGGGGC 7
 RESULT 595
 AAF20122/c
 ID AAF20122 standard; DNA; 10 BP.
 XX AC
 AC AAF20122;
 XX AC
 DT 14-MAR-2001 (first entry)
 XX
 DE Human adenosine A2b receptor polynucleotide fragment #1689.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.
 XX
 Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.
 XX
 PS Claim 14; Page 124; 1592pp; English.
 XX
 CC The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antiasthmatic, hypotensive and cyostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the

CC expression and or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention
 XX
 SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCGGGGC 9
 Db 9 GCGGGGC 3
 RESULT 596
 AAF19322
 ID AAF19322 standard; DNA; 10 BP.
 XX AC
 AC AAF19322;
 XX AC
 DT 14-MAR-2001 (first entry)
 XX
 DE Human adenosine A1 receptor polynucleotide fragment #889.
 XX
 KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
 KW human; airway disorder; bronchoconstriction; lung inflammation;
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cyostatic;
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
 KW cancer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200062736-A2.
 XX
 PD 26-OCT-2000.
 XX
 PF 24-MAR-2000; 2000WO-US008020.
 XX
 PR 06-APR-1999; 99US-0127958P.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 PA (NYCE/) NYCE J W.
 XX
 PI Nyce JW;
 XX
 XX WPI; 2000-679539/66.

PT Low adenosine (A) content antisense oligonucleotides which do not trigger
 PT adenosine receptors during metabolism, useful e.g. for treating cancers
 PT and respiratory obstructions.

XX Claim 14; Page 119; 1592pp; English.

XX The present invention describes low adenosine (A) content antisense
 CC oligonucleotides and compositions (I) comprising them. In the antisense
 CC oligonucleotides the A is replaced by a 'universal' or alternative base.
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
 CC immunosuppressive, antisthmatic, hypotensive and cytostatic activities.
 CC The antisense oligonucleotides and (I) can be used to down-regulate the
 CC expression and/or activity of target polypeptides associated with
 CC lung/respiratory disorders and malignancies, such as stimulating and
 CC activating peptide factors and transmitters, transcription factors,
 CC immunoglobulins and antibodies, antibody receptors, cytokines and
 CC chemokines, endogenously produced specific and non-specific enzymes,
 CC binding proteins, adhesion molecules and their receptors, cytokine and
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central
 CC nervous system (CNS) and peripheral nervous and non-nervous system
 CC receptors, CNS and peripheral nervous and non-nervous system peptide
 CC transmitters, defensins, growth factors, vasoactive peptides and
 CC receptors, binding proteins and malignancy associated proteins. The
 CC antisense oligonucleotides may be used in this way to treat disorders
 CC including respiratory obstruction (especially pulmonary obstruction
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or
 CC surfactant hypoproduction which are associated with a disease or
 CC condition selected from pulmonary vasoconstriction, inflammation,
 CC allergies, asthma, impeded respiration, respiratory distress syndrome
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide
 CC fragments and antisense oligonucleotides used in the exemplification of
 CC the present invention

SQ Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGGC 8
 DB 4 GCGCGGC 10

RESULT 597

AAA47487

ID AAA47487 standard; DNA; 10 BP.

AC AAA47487;

XX 20-OCT-2000 (first entry)

DE NotI adapter sequence.

XX TANGO; 128; 140; 197; 212; 213; 224; 239; modulating agent; asthma;
 KW graft versus-host diseases; rheumatoid arthritis; psoriasis;
 KW inflammatory bowel disease; septic shock; ulcerative colitis;
 KW Crohn's disease; chronic myelogenous leukemia; cancer; liver disease;
 KW Hodgkin's disease; osteoarthritis; Lyme's disease; cachexia;
 KW autoimmune disease; myasthenia gravis; autoimmune diabetes;
 KW systemic lupus erythematosus; transgenic animal; diagnosis; prognosis;
 KW prophylactic; therapeutic; ss.

OS Synthetic.

XX WO200039284-A1.

PN 06-JUL-2000.

XX 23-DEC-1999; 99WO-US031025.

XX 30-DEC-1998; 98US-00223546.
 PR (MILL-) MILLENNIUM PHARM INC.

XX Holtzman DA;

XX WPI; 2000-465743/40.

XX Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224
 PT and 239 polypeptides useful for the treatment of asthma, rheumatoid
 PT arthritis, psoriasis and autoimmune diseases.

XX Disclosure; Page 20; 209pp; English.

CC Nucleic acids encoding TANGO polypeptides are useful as modulating agents
 CC for regulating cellular processes like asthma, graft versus-host
 CC diseases, rheumatoid arthritis, psoriasis, inflammatory bowel disease,
 CC septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous
 CC leukemia, cancer, liver disease, Hodgkin's disease, osteoarthritis,
 CC Lyme's disease, cachexia and autoimmune diseases e.g. myasthenia gravis,
 CC autoimmune diabetes and systemic lupus erythematosus. The nucleic acids
 CC are also useful for producing transgenic animals and the TANGO
 CC polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239
 CC sequences are useful in forensic biology, for diagnostic assays,
 CC prognostic assays, pharmacogenomics and for monitoring clinical trials.
 CC TANGO polypeptides are suitable for both prophylactic and therapeutic
 CC methods for treating a subject at risk of a disorder or having a disorder
 CC associated with aberrant TANGO expression. A wide range of cellular
 CC disorders can be treated

SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCGGC 11
 DB 1 GCGCGGC 7

RESULT 598

ABN80674/c

ID ABN80674 standard; DNA; 10 BP.

XX AC ABN80674;

XX 15-JUL-2002 (first entry)

XX Universal high frequency bacterial PCR primer #5.

XX Primer; probe; affinity purification; cloning; biosynthetic pathway;
 KW hybridization screening; restriction endonuclease; universal; PCR; ss.

XX Synthetic.

XX WO200112861-A1.

XX 22-FEB-2001.

XX 18-AUG-2000; 2000WO-US022743.

XX 19-AUG-1999; 99US-0149788P.

XX 19-SEP-1999; 99US-0149822P.

XX (OMNI-) OMNISCIENCE PHARM.

XX Fomenkov A, Huang Y, Chaparian MG, Zheng S;

XX WPI; 2001-211237/21.

PT New primers and probes useful for targeted cloning and enrichment of

PT genes and gene clusters for affinity purification of genes or in cloning
 XX associated biosynthetic pathway genes.

PS Disclosure; Page 26; 74pp; English.

CC The invention relates to a set of novel primers and probes. The genes
 CC cloned are used in affinity purification of genes, and for cloning
 CC associated biosynthetic pathway genes. The gene probes/primers may be
 CC used in the discovery and characterization of bioactive compound coding
 CC sequences and gene clusters, as well as in the discovery of either single
 CC genes or entire clusters of adjacent genes involved in the total
 CC synthesis of compounds of interest, e.g. secondary metabolite
 CC biosynthetic pathways the products of which comprise very useful
 CC libraries for antibiotic and other therapeutic compound screening. The
 CC cloned genes are further useful for hybridization screening. The sequence
 CC represents a universal high frequency bacterial CDS decamer PCR primer
 XX
 SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCGCGC 11
 Db 10 GGCGCGC 4

RESULT 599

ABN80673/C

ID ABN80673 standard; DNA; 10 BP.

AC ABN80673;

DT 15-JUL-2002 (first entry)

XX Universal high frequency bacterial PCR primer #4.

KW Primer; probe; affinity purification; cloning; biosynthetic pathway;
 KW hybridization screening; restriction endonuclease; universal; PCR; ss.
 XX Synthetic.

PN WO200112861-A1.

PD 22-FEB-2001.

PF 18-AUG-2000; 2000WO-US022743.

PR 19-AUG-1999; 99US-0149788P.

PR 19-SEP-1999; 99US-0149822P.

PA (OMNI-) OMNISCIENCE PHARM.

PI Fomenkov A, Huang Y, Chaparian MG, Zheng S;

DR WPI; 2001-211237/21.

PT New primers and probes useful for targeted cloning and enrichment of
 PT genes and gene clusters for affinity purification of genes or in cloning
 PT associated biosynthetic pathway genes.

PS Disclosure; Page 26; 74pp; English.

CC The invention relates to a set of novel primers and probes. The genes
 CC cloned are used in affinity purification of genes, and for cloning
 CC associated biosynthetic pathway genes. The gene probes/primers may be
 CC used in the discovery and characterization of bioactive compound coding
 CC sequences and gene clusters, as well as in the discovery of either single
 CC genes or entire clusters of adjacent genes involved in the total
 CC synthesis of compounds of interest, e.g. secondary metabolite
 CC biosynthetic pathways the products of which comprise very useful
 CC libraries for antibiotic and other therapeutic compound screening. The

CC cloned genes are further useful for hybridization screening. The sequence
 CC represents a universal high frequency bacterial CDS decamer PCR primer
 XX
 SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGCGCGC 11
 Db 10 GGCGCGC 4

RESULT 600

AAF90454

ID AAF90454 standard; DNA; 10 BP.

XX AAF90454;

DT 06-AUG-2001 (first entry)

DE Egr-1 binding site.

XX Promoter; Egr-1; transcription factor; human; vulnery; wound healing;
 KW dermatological; antiulcer; ds.

OS Mammalia.

XX WO200140460-A1.

XX 07-JUN-2001.

PF 30-NOV-2000; 2000WO-EP011997.

PR 01-DEC-1999; 99GB-00028430.

PA (GLAX) GLAXO GROUP LTD.

PI Braddock M, Campbell CJ;

DR WPI; 2001-374827/39.

PT Screening modulators of epidermal growth factor receptor-1 useful for
 PT wound healing, involves providing expression system that is regulated by
 PT Egr-1 and analyzing effect of compound on expression from system.

PS Disclosure; Page 5; 81pp; English.

CC The present sequence is that of an Egr-1 binding site that has the
 CC capability of conferring Egr-1 dependency upon a promoter. An Egr-1
 CC binding site in found within the promoter (see AAF90451) of the human Egr-
 CC -1 gene, and may be involved in autoregulation. Transcription factor Egr-
 CC 1 is a potential regulator of over 30 genes and plays a role in growth,
 CC development and differentiation. It is induced upon injury to the
 CC vascular endothelium. The Egr-1 promoter, its variants, or any other
 CC promoter that is regulatable by Egr-1, can be used in an expression
 CC system to screen for compounds capable of modulating Egr-1 expression.
 CC Such compounds are used as medicaments or in drug development programs,
 CC particularly in the identification of drugs for wound healing (claimed).
 CC Conditions that may be treated include dermal ulcers arising from
 CC ischaemia and neuropathy associated with diabetes, deep vein thrombosis,
 CC post-operative scarring associated with e.g. cataracts, skin graft
 CC procedures, burns, psoriasis, and tissue engineering. Identified
 CC compounds may also be useful to reduce scarring during wound healing,
 CC restenosis following percutaneous trans-luminal coronary angioplasty, to
 CC modulate vessel wall calcification, treat cancer or other cell
 CC proliferative disorders, inhibit fibrotic conditions, for e.g. pulmonary
 CC and liver fibrosis, and to prevent alopecia

SQ Sequence 10 BP; 0 A; 2 C; 7 G; 0 T; 0 U; 1 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

```

Best Local Similarity 77.8%; Pred. No. 3.4e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGC 11
Db 1 GCGGGCGGC 9

RESULT 601
AAH64280/c
ID AAH64280 standard; cDNA; 10 BP.
XX AC AAH64280;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 1120.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX PF New isolated polynucleotides, useful for identifying specific cell type,
XX PR such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 64; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the
XX CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGGGCGGC 11
Db 7 GCGGGCGGC 1

RESULT 602
AAH64083
ID AAH64083 standard; cDNA; 10 BP.
XX AC AAH64083;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 923.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.

```

```

KW Human; transcriptome; gene expression pattern; cancer; drug screening;
KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.
XX PF New isolated polynucleotides, useful for identifying specific cell type,
XX PR such as cancer cell, comprises transcriptomes expressed in particular
XX PT cell types.
XX PS Claim 13; Page 60; 94pp; English.
XX CC The present invention describes a method of identifying the type of cell
XX CC in a sample, involving determining which of the sequences AAH63161-
XX CC AAH64724 is expressed by the cell. The transcriptomes described in the
XX CC invention are cell-type specific, cancer specific or ubiquitously
XX CC expressed in humans. They can also be used to screen for drugs, reduce
XX CC cancer specific gene expression, standardise expression and restore the
XX CC function of a diseased cell or tissue. The present sequence is one of the
XX CC transcriptomes described in the exemplification of the invention
XX SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGCGGC 8
Db 3 GCGGGCGGC 9

RESULT 603
AAH64084
ID AAH64084 standard; cDNA; 10 BP.
XX AC AAH64084;
XX DT 20-SEP-2001 (first entry)
XX DE Human ubiquitously expressed transcriptome sequence SEQ ID NO: 924.
XX KW Human; transcriptome; gene expression pattern; cancer; drug screening;
XX KW cancer diagnosis; cell specific gene expression; ss.
XX OS Homo sapiens.
XX PN WO200138577-A2.
XX PD 31-MAY-2001.
XX PF 21-NOV-2000; 2000WO-US031922.
XX PR 24-NOV-1999; 99US-00448480.
XX PA (UYJO ) UNIV JOHNS HOPKINS.
XX PI Velculescu VE, Vogelstein B, Kinzler KW;
XX DR WPI; 2001-367706/38.

```


XX Human; transcriptome; gene expression pattern; cancer; drug screening;
 KW cancer diagnosis; cell specific gene expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2001138577-A2.
 XX
 PD 31-MAY-2001.
 XX
 XX 21-NOV-2000; 2000WO-US031922.
 PF
 XX 24-NOV-1999; 99US-00448480.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu VE, Vogelstein B, Kinzler KW;
 PI
 XX WPI; 2001-367706/38.
 DR
 XX New isolated polynucleotides, useful for identifying specific cell type,
 PT such as cancer cell, comprises transcriptomes expressed in particular
 PT cell types.
 XX
 PS Claim 13; Page 47; 94pp; English.
 XX
 XX The present invention describes a method of identifying the type of cell
 CC in a sample, involving determining which of the sequences AAH63161-
 CC AAH64724 is expressed by the cell. The transcriptomes described in the
 CC invention are cell-type specific, cancer specific or ubiquitously
 CC expressed in humans. They can also be used to screen for drugs, reduce
 CC cancer specific gene expression, standardise expression and restore the
 CC function of a diseased cell or tissue. The present sequence is one of the
 CC transcriptomes described in the exemplification of the invention
 XX
 SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGCGGC 8
 Db |||||
 7 GCGCGGC 1
 RESULT 607
 AAD20712
 ID AAD20712 standard; DNA; 10 BP.
 XX
 AC AAD20712;
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE Primer #4 used to detect human GPIBA gene polymorphism.
 XX
 XX Human; haplotyping; glycoprotein Ib (platelet) alpha protein; GPIBA;
 KW Bernard-Soulier syndrome; platelet-type von Willebrand disease; HIV;
 KW Alzheimer's disease; polymorphism; human immunodeficiency virus; primer;
 KW ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2001175065-A2.
 XX
 PD 11-OCT-2001.
 XX
 XX 03-APR-2001; 2001WO-US010671.
 PF
 XX 03-APR-2000; 2000US-0194341P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA

PI Bentivegna SC, Choi JY, Klieh SE, Koshy B, Parks KE;
 XX WPI; 2001-626427/72.
 XX
 XX New haplotypes of the glycoprotein Ib platelet alpha polypeptide gene are
 PT useful for diagnosis and drug discovery for treating Bernard Soulier
 PT syndrome, platelet-type von Willebrand disease, HIV and Alzheimer's
 PT disease.
 XX
 XX Claim 18; Page 14; 66pp; English.
 PS
 XX The invention relates to methods for haplotyping glycoprotein Ib
 CC (platelet) alpha polypeptide (GPIBA) gene of an individual. The method
 CC involves determining if the individual has one of the GPIBA haplotypes or
 CC haplotype pairs. The methods of the invention are useful for disease
 CC diagnosis and in the discovery and development of drugs for treating
 CC diseases associated with GPIBA activity e.g. Bernard-Soulier syndrome,
 CC platelet-type von Willebrand disease, HIV and Alzheimer's disease. The
 CC present sequence is a primer used for detecting human GPIBA gene
 CC polymorphisms
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGCGGC 8
 Db |||||
 4 GCGCGGC 10
 RESULT 608
 AAH32888/c
 ID AAH32888 standard; cDNA; 10 BP.
 XX
 AC AAH32888;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE LPS activated human monocyte expression gene cDNA tag SEQ:261.
 XX
 XX Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
 KW expressed sequence tag; diagnosis; human disease; treatment; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2001069993-A.
 XX
 PD 21-MAR-2001.
 XX
 XX 28-APR-2000; 2000JP-00131079.
 PF
 XX 08-JUL-1999; 99JP-00195103.
 PR
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 PA
 XX WPI; 2001-304369/32.
 DR
 XX LPS activated human monocyte expression gene group.
 PT
 XX
 XX Claim 19; Page 43; 52pp; Japanese.
 PS
 XX The present invention describes an lipopolysaccharide (LPS) activated
 CC human monocyte expression gene group consisting of the high-ranking 50
 CC genes of the highest expression among the genes expressed by human
 CC monocyte stimulated by LPS in which the cDNA of each gene has the base
 CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
 CC CATG-3' nearest to the polyA region. The gene group is useful for the
 CC development of new means for the diagnosis and the treatment of various
 CC human diseases in which human monocyte plays an important role. AAH32628
 CC to AAH32943 represent specifically claimed LPS activated human monocyte
 CC expression gene cDNA tags from the present invention. AAH32944 represents

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CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 7 GCGGGGC 1

RESULT 609
AAH32889
ID AAH32889 standard; cDNA; 10 BP.
XX
AC AAH32889;
XX
DT 13-AUG-2001 (first entry)
XX
DE LPS activated human monocyte expression gene cDNA tag SEQ.262.
XX
KW Human; LPS; lipopolysaccharide; monocyte expression gene; tag; EST;
KW expressed sequence tag; diagnosis; human disease; treatment; ss.
XX
OS Homo sapiens.
XX
PN JP2001069993-A.
XX
PD 21-MAR-2001.
XX
PF 28-APR-2000; 2000JP-00131079.
XX
PR 08-JUL-1999; 99JP-00195103.
XX
PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR WPI; 2001-304369/32.
XX
PT LPS activated human monocyte expression gene group.
XX
PS Claim 19; Page 43; 52pp; Japanese.
XX
CC The present invention describes an lipopolysaccharide (LPS) activated
CC human monocyte expression gene group consisting of the high-ranking 50
CC genes of the highest expression among the genes expressed by human
CC monocyte stimulated by LPS in which the cDNA of each gene has the base
CC sequence of (AAH32628 to AAH32677) continuous to the base sequence 5'-
CC CATG-3', nearest to the polyA region. The gene group is useful for the
CC development of new means for the diagnosis and the treatment of various
CC human diseases in which human monocyte plays an important role. AAH32628
CC to AAH32943 represent specifically claimed LPS activated human monocyte
CC expression gene cDNA tags from the present invention. AAH32944 represents
CC an LPS activated human monocyte expression gene cDNA sequence encoding
CC AAB98009, which are given in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCG 9
Db 3 GCGGGCG 9

RESULT 610
AAF34183/c
ID AAF34183 standard; DNA; 10 BP.
XX

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AC AAF34183;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:922.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 32; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 1 A; 4 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGGGCA 12
Db 8 GCGGGCA 2

RESULT 611

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AAF42380/c
ID  AAF42380 standard; DNA; 10 BP.
XX
AC  AAF42380;
XX
DT  23-MAR-2001  (first entry)
XX
DE  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:9119.
XX
KW  Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
OS  Saccharomyces cerevisiae.
XX
PN  WO200077214-A2.
XX
PD  21-DEC-2000.
XX
PF  14-JUN-2000; 2000WO-US016223.
XX
PR  16-JUN-1999; 99US-00335032.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Velculescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
PT  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
PS  Example; Page 325; 419pp; English.
XX
CC  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
SQ  Sequence 10 BP; 2 A; 4 C; 3 G; 1 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  10 GCATCGT 16
    |||||
DB  10 GCATCGT 4

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RESULT 612
AAF34736
ID  AAF34736 standard; DNA; 10 BP.
XX
AC  AAF34736;
XX
DT  23-MAR-2001  (first entry)
XX
DE  Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1475.
XX
KW  Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW  nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW  serial analysis of gene expression; antifungal; tag; identification;
KW  linker; PCR primer; ds.
XX
OS  Saccharomyces cerevisiae.
XX
PN  WO200077214-A2.
XX
PD  21-DEC-2000.
XX
PF  14-JUN-2000; 2000WO-US016223.
XX
PR  16-JUN-1999; 99US-00335032.
XX
PA  (UYJO ) UNIV JOHNS HOPKINS.
XX
PI  Velculescu V, Vogelstein B, Kinzler K;
XX  WPI; 2001-061874/07.
XX
PT  Yeast gene coding sequences comprising NORF genes with serial analysis of
PT  gene expression (SAGE) tags, useful for studying, monitoring and
PT  affecting phases of the cell cycle.
XX
PS  Example; Page 52; 419pp; English.
XX
CC  The present invention describes an isolated DNA molecule comprising a
CC  coding sequence of a yeast gene selected from a group of 745 NORF (not
CC  previously assigned open reading frame; or nonannotated ORF) genes
CC  comprising a SAGE (serial analysis of gene expression) tag. Also
CC  described are: (1) a method (M1) of using NORF genes to affect the cell
CC  cycle comprising administering a NORF gene whose expression varies by at
CC  least 10% between any two phases of the cell cycle selected from log
CC  phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC  antifungal drugs comprising: (a) contacting a test substance with a yeast
CC  cell; and (b) monitoring expression of a NORF gene whose expression
CC  varies as in M1, where a test substance which modifies the expression of
CC  the yeast gene is a candidate antifungal drug; (3) a method (M3) for
CC  identifying human genes which are involved in cell cycle progression
CC  comprising contacting human DNA with a probe which comprises at least 10
CC  contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC  and (4) a method (M4) for identifying a candidate drug as a member of a
CC  class of drugs having a characteristic effect on gene expression in a
CC  yeast cell comprising contacting a yeast cell with a candidate drug and
CC  monitoring expression in the yeast cell of at least 1 NORF gene whose
CC  expression is affected by the class of drugs. The NORF genes may be used
CC  to study, monitor and affect phases of the cell cycle, the differentially
CC  expressed genes may be used as markers of phases of the cell cycle. The
CC  methods may be used to identify candidate drugs which affect the cell
CC  cycle and for identification of antifungal drugs. AAF33268 to AAF44064
CC  represent SAGE tags used in the exemplification of the present invention.
CC  AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC  method, in the exemplification of the present invention
XX
SQ  Sequence 10 BP; 2 A; 3 C; 2 G; 3 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 10 GCATCGT 16
 Db 1 |||||
 1 GCATCGT 7

RESULT 613
 AAF33729/C
 ID AAF33729 standard; DNA; 10 BP.
 AC AAF33729;
 XX
 XX 23-MAR-2001 (first entry)
 DT
 DE
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:468.
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Claim 1; Page 392; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
 Db 7 CGGCATC 1

RESULT 614
 AAF35209/C
 ID AAF35209 standard; DNA; 10 BP.
 XX
 AC AAF35209;
 XX
 XX 23-MAR-2001 (first entry)
 DT
 DE
 XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1948.
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 PF
 XX 16-JUN-1999; 99US-00335032.
 PR
 XX (UYJO) UNIV JOHNS HOPKINS.
 PA
 XX Velculescu V, Vogelstein B, Kinzler K;
 PI WPI; 2001-061874/07.
 DR
 XX
 XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 69; 419pp; English.
 XX
 XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX

```
SQ Sequence 10 BP; 3 A; 3 C; 2 G; 2 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13
    |||||
Db 10 GCGGCAT 4

RESULT 615
AAF37089/c
ID AAF37089 standard; DNA; 10 BP.
XX
AC AAF37089;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:3828.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 136; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
```

```
CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
CC method, in the exemplification of the present invention
XX
SQ Sequence 10 BP; 5 A; 2 C; 2 G; 1 T; 0 U; 0 Other;
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GCATCGT 16
    |||||
Db 7 GCATCGT 1

RESULT 616
AAF41929/c
ID AAF41929 standard; DNA; 10 BP.
XX
AC AAF41929;
XX
DT 23-MAR-2001 (first entry)
XX
DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:8668.
XX
KW Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
KW serial analysis of gene expression; antifungal; tag; identification;
KW linker; PCR primer; ds.
XX
OS Saccharomyces cerevisiae.
XX
PN WO200077214-A2.
XX
PD 21-DEC-2000.
XX
PF 14-JUN-2000; 2000WO-US016223.
XX
PR 16-JUN-1999; 99US-00335032.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Velculescu V, Vogelstein B, Kinzler K;
XX WPI; 2001-061874/07.
XX
PT Yeast gene coding sequences comprising NORF genes with serial analysis of
PT gene expression (SAGE) tags, useful for studying, monitoring and
PT affecting phases of the cell cycle.
XX
PS Example; Page 309; 419pp; English.
XX
CC The present invention describes an isolated DNA molecule comprising a
CC coding sequence of a yeast gene selected from a group of 745 NORF (not
CC previously assigned open reading frame; or nonannotated ORF) genes
CC comprising a SAGE (serial analysis of gene expression) tag. Also
CC described are: (1) a method (M1) of using NORF genes to affect the cell
CC cycle comprising administering a NORF gene whose expression varies by at
CC least 10% between any two phases of the cell cycle selected from log
CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
CC antifungal drugs comprising: (a) contacting a test substance with a yeast
CC cell; and (b) monitoring expression of a NORF gene whose expression
CC varies as in M1, where a test substance which modifies the expression of
CC identifying human genes which are involved in cell cycle progression
CC comprising contacting human DNA with a probe which comprises at least 10
CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
CC and (4) a method (M4) for identifying a candidate drug as a member of a
CC class of drugs having a characteristic effect on gene expression in a
CC yeast cell comprising contacting a yeast cell with a candidate drug and
CC monitoring expression in the yeast cell of at least 1 NORF gene whose
CC expression is affected by the class of drugs. The NORF genes may be used
CC to study, monitor and affect phases of the cell cycle, the differentially
CC expressed genes may be used as markers of phases of the cell cycle. The
CC methods may be used to identify candidate drugs which affect the cell
CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
CC represent SAGE tags used in the exemplification of the present invention.
```

CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 GCATCGT 16
 |||||
 Db 8 GCATCGT 2
 RESULT 617
 AAF43170/C
 ID AAF43170 standard; DNA; 10 BP.
 XX AAF43170;
 AC
 XX
 XX 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:11309.
 XX
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; db.
 XX
 XX Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 353; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose

CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 5 C; 2 G; 3 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GCGGCA 12
 |||||
 Db 7 GCGGCA 1
 RESULT 618
 AAF40066/C
 ID AAF40066 standard; DNA; 10 BP.
 XX AAF40066;
 AC
 XX
 XX 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6805.
 XX
 XX Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; db.
 XX
 XX Saccharomyces cerevisiae.
 XX
 XX WO200077214-A2.
 XX
 XX 21-DEC-2000.
 XX
 XX 14-JUN-2000; 2000WO-US016223.
 XX
 XX 16-JUN-1999; 99US-00335032.
 XX
 XX (UYJO) UNIV JOHNS HOPKINS.
 XX
 XX Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 XX
 PT Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.
 XX
 XX Example; Page 243; 419pp; English.
 XX
 CC The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a

CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 1 A; 6 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
 |||||
 Db 10 GGGCGGC 4

RESULT 619
 AAF34402/c
 ID AAF34402 standard; DNA; 10 BP.

XX AAF34402;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:1141.

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 40; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression

CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF4064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 4 A; 2 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
 |||||
 Db 7 CGGCATC 1

RESULT 620
 AAF39330/c
 ID AAF39330 standard; DNA; 10 BP.

XX AAF39330;

XX 23-MAR-2001 (first entry)

XX Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:6069.

XX Yeast; Saccharomyces cerevisiae; Characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.

XX Saccharomyces cerevisiae.

OS WO200077214-A2.

PN 21-DEC-2000.

XX 14-JUN-2000; 2000WO-US016223.

PF 16-JUN-1999; 99US-00335032.

XX (UYJO) UNIV JOHNS HOPKINS.

XX Velculescu V, Vogelstein B, Kinzler K;

XX WPI; 2001-061874/07.

XX Yeast gene coding sequences comprising NORF genes with serial analysis of
 PT gene expression (SAGE) tags, useful for studying, monitoring and
 PT affecting phases of the cell cycle.

XX Example; Page 216; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log
 CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression

CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 2 A; 2 C; 2 G; 4 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 10 GCATCGT 16
 Db 7 GCATCGT 1

RESULT 621
 AAF40942/C
 ID AAF40942 standard; DNA; 10 BP.
 AC AAF40942;
 XX
 DT 23-MAR-2001 (first entry)
 XX
 DE Yeast NORF gene SAGE tag oligonucleotide SEQ ID NO:7681.
 XX
 KW Yeast; Saccharomyces cerevisiae; characterisation; cell cycle; NORF;
 KW nor previously assigned open reading frame; nonannotated ORF; SAGE;
 KW serial analysis of gene expression; antifungal; tag; identification;
 KW linker; PCR primer; ds.
 XX
 OS Saccharomyces cerevisiae.
 XX
 PN WO200077214-A2.
 XX
 PD 21-DEC-2000.
 XX
 PF 14-JUN-2000; 2000WO-US016223.
 XX
 PR 16-JUN-1999; 99US-00335032.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI Velculescu V, Vogelstein B, Kinzler K;
 XX WPI; 2001-061874/07.
 DR
 XX

Yeast gene coding sequences comprising NORF genes with serial analysis of
 gene expression (SAGE) tags, useful for studying, monitoring and
 affecting phases of the cell cycle.

Example; Page 274; 419pp; English.

XX The present invention describes an isolated DNA molecule comprising a
 CC coding sequence of a yeast gene selected from a group of 745 NORF (not
 CC previously assigned open reading frame; or nonannotated ORF) genes
 CC comprising a SAGE (serial analysis of gene expression) tag. Also
 CC described are: (1) a method (M1) of using NORF genes to affect the cell
 CC cycle comprising administering a NORF gene whose expression varies by at
 CC least 10% between any two phases of the cell cycle selected from log

CC phase, S phase and G2/M; (2) a method (M2) for screening candidate
 CC antifungal drugs comprising: (a) contacting a test substance with a yeast
 CC cell; and (b) monitoring expression of a NORF gene whose expression
 CC varies as in M1, where a test substance which modifies the expression of
 CC the yeast gene is a candidate antifungal drug; (3) a method (M3) for
 CC identifying human genes which are involved in cell cycle progression
 CC comprising contacting human DNA with a probe which comprises at least 10
 CC contiguous nucleotides of a NORF gene whose expression varies as in M1;
 CC and (4) a method (M4) for identifying a candidate drug as a member of a
 CC class of drugs having a characteristic effect on gene expression in a
 CC yeast cell comprising contacting a yeast cell with a candidate drug and
 CC monitoring expression in the yeast cell of at least 1 NORF gene whose
 CC expression is affected by the class of drugs. The NORF genes may be used
 CC to study, monitor and affect phases of the cell cycle, the differentially
 CC expressed genes may be used as markers of phases of the cell cycle. The
 CC methods may be used to identify candidate drugs which affect the cell
 CC cycle and for identification of antifungal drugs. AAF33268 to AAF44064
 CC represent SAGE tags used in the exemplification of the present invention.
 CC AAF33262 to AAF33267 represent linkers and PCR primers used in the SAGE
 CC method, in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 7 C; 2 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGCGG 7
 Db 7 CGCGCGG 1

RESULT 622
 AAS99952
 ID AAS99952 standard; DNA; 10 BP.
 XX
 AC AAS99952;
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Even-skipped homeobox 1 (EVX1) gene allele-specific oligonucleotide #29.
 XX
 KW Even-skipped homeo box 1; EVX1; neurological disease; drug screening;
 KW haplotyping; single nucleotide polymorphism; SNP; human; ss;
 KW allele-specific oligonucleotide.
 XX
 OS Homo sapiens.
 XX
 PN WO200190120-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 21-MAY-2001; 2001WO-US016559.
 XX
 PR 19-MAY-2000; 2000US-0205437P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Duda A, Klieem SE, Kumar AM;
 XX WPI; 2002-089913/12.
 DR
 XX Novel genetic variants of even-skipped homeo box 1, EVX1 gene useful for
 PT therapeutic purposes and for expressing EVX1 protein useful in
 PT identifying drugs to treat neurological diseases.
 XX
 PS Claim 18; Page 13; 69pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (I), comprising a
 CC nucleotide sequence which is a polymorphic variant of a reference
 CC sequence for the even-skipped homeo box 1 (homologue of Drosophila)
 CC (EVX1) gene or its fragment, or a polymorphic variant of a reference
 CC sequence for a EVX1 cDNA or its fragment. EVX1 polypeptide (II) is useful

CC for screening for drugs targeting the polypeptide, by contacting the EVX1
 CC polymorphic variant with a candidate agent and assaying for binding
 CC activity. A method is described for identifying an association between a
 CC trait such as a clinical response to a drug targeting EVX1 and a
 CC haplotype or haplotype pair of EVX1 gene. The methods are useful in
 CC developing diagnostic tests and therapeutic treatments for neurological
 CC diseases. (I) is useful for studying the expression and function of EVX1
 CC and expressing EVX1 protein for use in screening for candidate drugs to
 CC treat diseases related to EVX1 activity. The polymorphism and haplotype
 CC data are useful for validating whether EVX1 is a suitable target for
 CC drugs to treat neurological diseases, screening for such drugs and
 CC reducing bias in clinical trials of such drugs. (I) is useful for
 CC therapeutic purposes. (I) is useful for determining if an individual has
 CC one of the haplotypes 1-4 or the haplotype pairs. Establishing the EVX1
 CC haplotype or haplotype pair of an individual is useful for improving the
 CC efficiency and reliability of several steps in the discovery and
 CC development of drugs for treating diseases associated with EVX1 activity
 CC e.g. neurological diseases. The haplotyping method is useful to validate
 CC EVX1 as a candidate target for treating a specific condition or disease
 CC predicted to be associated with EVX1 activity. (I) is useful for studying
 CC expression of the EVX1 isogenes in vivo, for in vivo screening and
 CC testing of drugs against EVX1 protein and for testing the efficacy of
 CC therapeutic agents and compounds for neurological diseases in a
 CC biological system. Antibody raised against (II) is useful for diagnostic
 CC and prognostic formats and therapeutic methods, for immunoprecipitating
 CC (II) from solution, for detecting EVX1 protein isoforms in biological
 CC samples, frozen tissue sections, cells which have been fixed or unfixed
 CC and prepared on slides, for use in immunocytochemical,
 CC immunohistochemical and immunofluorescence techniques. AAS99924-AAS99958
 CC represent human EVX1 gene allele-specific oligonucleotides of the
 CC invention
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GCGGGCG 9
 Db 1 GCGGGCG 7
 |||||

RESULT 623
 ABL52168/c
 ID ABL52168 standard; DNA; 10 BP.
 AC ABL52168;
 XX
 XX 12-JUL-2002 (first entry)
 XX
 DE Human PER1 preferred oligonucleotide primer SEQ ID NO:93.
 XX
 XX Human; period (Drosophila) homologue 1; PER1; polymorphic variant;
 KW polymorphic site; genotyping; haplotyping; circadian rhythm regulation;
 KW single nucleotide polymorphism; SNP; Gene; primer; ss.
 XX
 OS Homo sapiens.
 XX
 XX WO200222650-A2.
 PN
 XX 21-MAR-2002.
 PD
 XX 13-SEP-2001; 2001WO-US028780.
 PF
 XX 13-SEP-2000; 2000US-0232468P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Duda A, Kiem SE, Koshy B;
 PI WPI; 2002-393941/42.
 XX
 XX

PT Novel isolated human period Drosophila homolog 1 polynucleotide, useful
 PT for therapeutic purposes, for studying the expression and function of the
 PT polynucleotide, and for expressing the homolog.
 XX

Claim 19; Page 15; 162pp; English.

XX The present invention describes an isolated human period (Drosophila)
 CC homologue 1, (PER1) polynucleotide (I) comprising a sequence which is a
 CC polymorphic variant for a reference sequence (ABLS2077) for the PER1 gene
 CC or its fragment, or a polymorphic variant of a reference sequence
 CC (ABLS2078) for a PER1 cDNA or its fragment. The present invention also
 CC describes methods for genotyping and haplotyping the PER1 gene of an
 CC individual. (I) is useful in studying the expression and function of
 CC PER1, and in expressing PER1 protein for use in screening for candidate
 CC drugs to treat diseases related to PER1 activity. (I) is useful for
 CC therapeutic purposes. A recombinant non-human organism transformed or
 CC transfected with (I) can be used for studying expression of the PER1
 CC isogenes in vivo, for in vivo screening and testing of drugs targeted
 CC against PER1 protein, and for testing the efficacy of therapeutic agents
 CC and compounds for disorders associated with circadian rhythm regulation.
 CC The present sequence represents a preferred oligonucleotide primer for
 CC human PER1, which is used in the exemplification of the present invention
 XX
 SQ Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGG 10
 Db 9 CGGGCGG 3
 |||||

RESULT 624

ABK95853
 ID ABK95853 standard; DNA; 10 BP.
 XX
 AC ABK95853;
 XX
 XX 24-SEP-2002 (first entry)
 XX
 DE Solute Carrier Family 1 (SLC1A4) primer extension oligonucleotide #24.
 XX
 KW Solute carrier family 1; SLC1A4; haplotyping; human; cancer; primer;
 KW glutamate/neutral amino acid transporter; neurological disease; PCR; ss;
 KW amino acid transporter disorder; single nucleotide polymorphism; SNP.
 XX
 OS Homo sapiens.
 XX
 XX WO200244198-A2.
 PN
 XX 06-JUN-2002.
 PD
 XX 29-NOV-2001; 2001WO-US044781.
 PF
 XX 30-NOV-2000; 2000US-0250254P.
 PR
 XX (GENA-) GENAISSANCE PHARM INC.
 PA
 XX Bieglecki KM, Kazemi A, Russo DP, Sausker EA;
 PI WPI; 2002-519580/55.
 XX
 XX Novel genetic variants of Solute Carrier Family 1 (Glutamate/Neutral
 PT Amino Acid Transporter), Member 4 isogenes, for improving efficiency and
 PT reliability in drug development for treating cancers.
 XX
 PS Claim 17; Page 16; 139pp; English.
 XX
 CC The invention relates to an isolated polynucleotide (I) comprising a
 CC first nucleotide sequence which comprises solute carrier family 1
 CC (glutamate/neutral amino acid transporter), member 4 (SLC1A4) isogenes

CC (II) and an isolated polypeptide (III) comprising an amino acid sequence
 CC which is a polymorphic variant of a reference sequence for SLC1A4
 CC protein. Also described are methods for: (1) haplotyping or genotyping
 CC SLC1A4 gene of an individual; (2) predicting a haplotype pair for SLC1A4
 CC gene of an individual; (3) identifying an association between a trait and
 CC at least one haplotype or haplotype pair of SLC1A4 gene. (III) is useful
 CC in screening for drugs targeting (III) that are useful for treating
 CC cancer, neurological diseases and amino acid transporter disorders. The
 CC methods are useful for improving the efficiency and reliability of
 CC several steps in the discovery and development of drugs for treating
 CC diseases associated with SLC1A4 activity. The haplotyping method is also
 CC used by the pharmaceutical research scientist to validate SLC1A4 as a
 CC candidate target for treating a specific condition or disease predicted
 CC to be associated with SLC1A4 activity, e.g. cancer, neurological diseases
 CC and amino acid transporter disorders, and in the design of clinical
 CC trials for treating a specific condition of disease associated with
 CC SLC1A4 activity. The methods are also useful for screening compounds
 CC targeting SLC1A4. Anti-SLC1A4 antibody is useful in diagnostic,
 CC prognostic and therapeutic methods. ABK95761-ABK95877 represent SLC1A4
 CC gene allele-specific oligonucleotides, primer extension oligonucleotides
 CC and related PCR primers used to identify single nucleotide polymorphisms
 CC (SNP) of the gene
 CC
 XX

SQ Sequence 10 BP; 2 A; 2 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCG 15
 Db 2 GGCATCG 8
 |||||

RESULT 625

ID ABK96067 standard; DNA; 10 BP.

XX AC ABK96067;

XX 24-SEP-2002 (first entry)

DE Human LIPE gene polymorphism detection oligonucleotide primer #42.

XX Human; lipase; hormone sensitive; LIPE; isogene; obesity; male sterility;
 KW polymorphism; primer; ss.

XX Homo sapiens.

XX WO200240502-A2.

XX 23-MAY-2002.

XX 16-NOV-2001; 2001WO-US043518.

XX 16-NOV-2000; 2000US-0249302P.

XX (GENA-) GENAISSANCE PHARM INC.

XX Anastasio AE, Bentivegna SC, Chew A, Koshiy B, Rounds E;

XX WPI; 2002-519369/55.

XX Novel genetic variants of Lipase. Hormone-Sensitive isogenes, useful for
 PT improving efficiency and reliability in drug development for treating
 PT diseases associated with LIPE activity, e.g. obesity and male sterility.

XX Claim 17; Page 16; 142pp; English.

XX The present invention relates to a new polynucleotide comprising a
 CC nucleotide sequence which comprises lipase, hormone sensitive (LIPE)
 CC isogenes. The invention is useful in screening for drugs targeting LIPE
 CC isogenes that are useful for treating obesity and male sterility. The

CC methods of the invention are useful for improving the efficiency and
 CC reliability of several steps in the discovery and development of drugs
 CC for treating diseases associated with LIPE activity. The polynucleotide
 CC is useful in studying the expression and function of LIPE, and in
 CC expressing LIPE protein for use in screening for candidate drugs to treat
 CC diseases related to LIPE activity. It is also useful in studying the
 CC effect of the variation on the biological activity of LIPE as well as on
 CC the binding affinity of candidate drugs targeting LIPE for the treatment
 CC of obesity and male sterility. The invention is useful for studying the
 CC expression of LIPE isogenes in vivo, for in vivo screening and testing of
 CC drugs targeted against LIPE protein, and for testing the efficacy of
 CC therapeutic agents and compounds for treating obesity and male sterility
 CC in a biological system. The present nucleic acid sequence represents one
 CC of a collection (ABK96026-ABK96083) of oligonucleotide primers that were
 CC used in the invention to detect polymorphisms in the human LIPE gene
 XX

SQ Sequence 10 BP; 3 A; 3 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
 Db 3 GCGCGCA 9
 |||||

RESULT 626

ID AAS96206 standard; DNA; 10 BP.

XX AC AAS96206;

XX 26-FEB-2002 (first entry)

DE Human Acetylcholinesterase gene ASO primer extension primer #24.

XX Human; ss; PCR primer; allele specific oligonucleotide; ASO; ACHS;
 KW acetylcholinesterase; polymorphic variant; haplotyping; genotyping;
 KW neurological disease; Parkinson's disease; Alzheimer's disease; cancer;
 KW leukaemia; tumour; chromosome 7q22; primer extension.

XX Homo sapiens.

XX WO200179219-A2.

XX 25-OCT-2001.

XX 11-APR-2001; 2001WO-US011853.

XX 14-APR-2000; 2000US-0197173P.

XX (GENA-) GENAISSANCE PHARM INC.

XX (KAZE/) KAZEMI A.

XX Bentivegna SC, Chew A, Choi JY, Koshiy B;

XX WPI; 2002-055248/07.

XX New polymorphic variants comprising acetylcholinesterase (ACHE) isogene,
 PT useful in expressing ACHE protein for use in screening for candidate
 PT drugs to treat diseases related to ACHE activity, e.g. neurological
 PT diseases or cancer.

XX Claim 18; Page 14; 79pp; English.

XX The invention relates to a polynucleotide comprising a polymorphic
 CC variant of an acetylcholinesterase (ACHE) gene or fragment, protein or
 CC complement, the variant comprising an ACHE isogene defined by a haplotype
 CC selected from haplotypes 1-20 listed in the specification. Also included
 CC are methods for haplotyping and genotyping the ACHE gene of an
 CC individual, a method for predicting a haplotype pair for the ACHE gene of
 CC an individual, a method for identifying an association between a trait

CC and at least one haplotype or haplotype pair of ACH gene, recombinant
 CC nonhuman organisms transformed or transfected with the polynucleotide
 CC where the organism expresses ACH protein encoded by the first nucleotide
 CC sequence or encoded by the polymorphic variant sequence, an isolated
 CC antibody specific for and immunoreactive with ACH, a method of screening
 CC for drugs targeting the polypeptide contacting ACH polymorphic variant
 CC with a candidate agent and assaying for binding activity, a computer
 CC system for storing and analysing polymorphism data for ACH gene and a
 CC genome anthology for ACH gene which comprises ACH isogenes defined by
 CC haplotypes 1-20 given in the specification. The Polymorphisms are useful
 CC for studying the biological function of ACH as well as in identifying
 CC drugs targeting this protein for the treatment of disorder related to its
 CC abnormal expression or function. The polymorphic variants may also be
 CC used in screening for compounds targeting ACH to treat a specific
 CC condition or disease predicted to be associated with ACH activity e.g.
 CC neurological diseases (e.g. Parkinson's disease and Alzheimer's disease),
 CC cancer, leukaemia, and tumours. The ACH gene maps to human chromosome
 CC 7q22. The present sequence is the allele specific (ASO) portion of a PCR
 CC primer used in a primer extension experiment to detect the polymorphic
 CC ACH variants of the invention
 CC
 XX

SQ Sequence 10 BP; 0 A; 5 C; 4 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7
 |||||
 Db 8 CGGCGGG 2

RESULT 627

ABK81360
 ID ABK81360 standard; DNA; 10 BP.

AC ABK81360;

DT 13-AUG-2002 (first entry)

DE Human FOS gene allele-specific oligonucleotide PCR primer #3.

KW Human; v-fos FBJ murine osteosarcoma viral oncogene homologue; FOS; PCR;
 KW cytostatic; gene therapy; single nucleotide polymorphism; haplotyping;
 KW haplotype pair; developmental bone disorder; cancer; tumour; ss; primer;
 KW chromosome 14q21-q31.

XX Homo sapiens.

XX WO200232931-A2.

PN 25-APR-2002.

PF 19-OCT-2001; 2001WO-US046142.

PR 19-OCT-2000; 2000US-0241620P.

PA (GENA-) GENAISANCE PHARM INC.

PI Anastasio AE, Kliem SE, Koshy B, Lee HH;

XX WPI; 2002-435529/46.

XX Novel genetic variants of V-Fos FBJ Murine Osteosarcoma Viral Oncogene
 PT Homolog (FOS) isogenes, useful for improving efficiency and reliability
 PT in drug development for treating developmental bone disorders.

PS Claim 17; Page 14; 73pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene
 CC encoding the human v-fos FBJ murine osteosarcoma viral oncogene homologue
 CC (FOS) polypeptide. A method for haplotyping the FOS gene in an individual
 CC comprises identifying the nucleotide at one or more polymorphic sites and

CC determining whether one of the copies of the gene is defined by one of
 CC the FOS haplotypes given in the specification or whether both copies are
 CC defined by a haplotype pair. This method is useful in genotyping, whereby
 CC all possible haplotype pairs can be assigned to specific genotypes. An
 CC association between a trait and a haplotype or haplotype pair of the FOS
 CC gene can be identified by comparing the frequency of the haplotype or
 CC haplotype pair in a population exhibiting the trait with the frequency of
 CC the haplotype or haplotype pair in a reference population, where a higher
 CC haplotype frequency in the trait population indicates the trait is
 CC associated with the haplotype or haplotype pair. FOS and its
 CC corresponding DNA are used for studying the expression and function of
 CC FOS, for use in screening for candidate drugs to treat diseases related
 CC to FOS activity, such as developmental bone disorders and tumours. The
 CC sequences are also useful for studying the effect of variation on the
 CC biological activity of FOS as well as on the binding affinity of
 CC candidate drugs targeting FOS. Sequences ABK81358-ABK81377 represent
 CC allele-specific oligonucleotide PCR primers used for detecting FOS gene
 CC polymorphisms
 CC

XX Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
 SQ

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGCGGG 10
 |||||
 Db 4 CGGCGGG 10

RESULT 628

ABQ71649
 ID ABQ71649 standard; DNA; 10 BP.

XX AC ABQ71649;

XX 28-AUG-2002 (first entry)

XX Zinc finger protein related oligonucleotide target SEQ ID NO:1641.

XX Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.

XX Synthetic.

XX WO200242459-A2.

XX 30-MAY-2002.

XX 20-NOV-2001; 2001WO-US043438.

XX 20-NOV-2000; 2000US-00716637.

XX (SANG-) SANGAMO BIOSCIENCES INC.

XX Liu Q;

XX WPI; 2002-500284/53.

XX New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 51; 81pp; English.

XX The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (I1) comprising (I); (2) a polynucleotide (I11) encoding (I) or (I1); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it

CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is
 CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
 |||||
 Db 3 GCGCGCA 9

RESULT 629
 ABQ71648
 ID ABQ71648 standard; DNA; 10 BP.
 XX
 AC ABQ71648;
 XX
 DT 28-AUG-2002 (first entry)
 XX
 DE Zinc finger protein related oligonucleotide target SEQ ID NO:1640.
 XX
 KW Zinc finger protein; ZFP; DNA binding protein; zinc finger; ss.

XX Homo sapiens.
 OS Synthetic.
 XX WO200242459-A2.
 XX 30-MAY-2002.
 XX
 XX 20-NOV-2001; 2001WO-US043438.
 XX
 XX 20-NOV-2000; 2000US-00716637.
 XX (SANG-) SANGAMO BIOSCIENCES INC.
 PA
 PI Liu Q;
 XX
 DR WPI; 2002-500284/53.
 XX

PT New zinc finger protein that binds to target site, useful in studying
 PT gene function and for human therapeutics and plant engineering, comprises
 PT first, second and third zinc fingers, ordered from N- to C-terminus.

PS Example 1; Page 51; 81pp; English.
 XX
 CC The present invention describes a zinc finger protein (I) that binds to a
 CC target site, comprising a first (F1), a second (F2), and a third (F3)
 CC zinc finger, ordered F1, F2, F3 from N-terminus to C-terminus, where the
 CC target site comprises, in 3'-5' direction, a first (S1), a second (S2),
 CC and a third (S3) target subsite. Also described are: (1) a polypeptide
 CC (I) comprising (I); (2) a polynucleotide (III) encoding (I) or (II); and
 CC (3) designing (M) (I) involves selecting the F1 zinc finger such that it
 CC binds to the S1 target subsite, selecting the F2 zinc finger such that it
 CC binds to the S2 target subsite, and selecting the F3 zinc finger such
 CC that it binds to the S3 target subsite, thus designing (I) that binds to
 CC a target site. (I) is useful for recognition of triplet target subsites
 CC having the nucleotide G in the 5'-most position of the subsite. (I) is

CC useful in studying gene function, and for human therapeutics and plant
 CC engineering. (I), (II) or (III) is useful in therapeutic methods to
 CC modulate the expression of a target region within a subject, in
 CC diagnostic methods for sequence specific detection of target nucleic acid
 CC in a sample, and in assays to determine the phenotype and function of
 CC gene expression. (I) has improved affinity and specificity for their
 CC target sequences, as well as enhanced biological activity. ABQ71213 to
 CC ABQ72214 and ABP48191 to ABP51230 represent DNA target sequences and zinc
 CC finger peptides which are given in the exemplification of the present
 CC invention

XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
 |||||
 Db 3 GCGCGCA 9

RESULT 630
 ABA98376
 ID ABA98376 standard; DNA; 10 BP.
 XX
 AC ABA98376;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE SCN2B gene polymorphisms oligonucleotide primer #2.
 XX
 KW Human; sodium channel voltage gated type 2 beta polypeptide; SCN2B; ds;
 KW gene therapy; neuroprotective; demyelinating disease.
 XX
 OS Homo sapiens.

XX WO200179547-A1.
 XX 25-OCT-2001.
 XX
 XX 03-APR-2001; 2001WO-US010743.
 XX
 XX 13-APR-2000; 2000US-0196597P.
 XX (GENA-) GENAISSANCE PHARM INC.
 XX
 XX Chew A, Choi JY, Koshy B;
 XX WPI; 2002-075072/10.

XX
 PT New polynucleotide containing polymorphisms in the human sodium channel
 PT voltage gated type 2 beta polypeptide (SCN2B) gene, for developing drugs
 PT for treating demyelinating diseases.

PS Claim 17; Page 13; 63pp; English.

XX
 CC This invention relates to an isolated polynucleotide which is a
 CC polymorphic variant of a reference sequence for sodium channel voltage
 CC gated type 2 beta polypeptide (SCN2B) gene. The methods have
 CC applicability in developing diagnostic tests and therapeutic treatments
 CC for demyelinating diseases. The protein is useful for studying the
 CC expression and function of SCN2B and expressing SCN2B protein for use in
 CC screening for candidate drugs to treat diseases related to SCN2B
 CC activity. The polymorphism and haplotype data are useful for validating
 CC whether SCN2B is a suitable target for drugs to treat demyelinating
 CC diseases, screening for such drugs and reducing bias in clinical trials.
 CC The haplotyping method is useful to validate SCN2B as a candidate target
 CC for treating a specific condition or disease predicted to be associated
 CC with SCN2B activity. A recombinant non-human organism transformed or
 CC transfected with the polypeptide is useful for studying expression of the
 CC SCN2B isogenes in vivo, for in vivo screening and testing of drugs
 CC against SCN2B protein and for testing the efficacy of therapeutic agents

CC and compounds for demyelinating diseases in a biological system. This
 CC sequence is used during the detection of polymorphisms of the SCN2B gene
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGCGC 8

DB 4 GGCGGCGC 10

RESULT 631

AAD25219
 ID AAD25219 standard; DNA; 10 BP.

XX AC AAD25219;

DT 12-MAR-2002 (first entry)

DE Human homeo box D3 (HOXD3) gene polymorphism detecting primer #18.

XX Human; homeo box D3; HOXD3; polymorphism; developmental disorder;
 KW haplotype; HT; allele-specific oligonucleotide; ASO; tumour; therapy;
 KW drug screening; cytostatic; primer; ss.

XX OS Homo sapiens.

PN WO200190127-A2.

XX PD 29-NOV-2001.

PF 24-MAY-2001; 2001WO-US016982.

XX PR 25-MAY-2000; 2000US-0207076P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Duda A, Kazemi A, Koshy B, Kumar AM;

XX WPI; 2002-075363/10.

DR New genetic variants of Homeo Box D3 for studying expression and function
 of the protein, and for screening drugs to treat diseases e.g.
 PT developmental disorders and tumors.

PS Claim 18; Page 13; 66pp; English.

XX The invention relates to genetic variants of the homeo box D3 (HOXD3)
 CC gene. HOXD3 gene includes 9 polymorphic sites PS1-PS9. Haplotypes (HTS)
 CC or haplotype pairs (HP) for PS1-PS9 in the HOXD3 gene are useful for
 CC improving the efficiency and reliability of several steps in the
 CC discovery and development of drugs for treating diseases associated with
 CC HOXD3 activity, e.g., developmental disorders and tumours. HOXD3 isogene
 CC is useful in studying the expression and function of HOXD3 and in
 CC expressing HOXD3 protein for use in screening for candidate drugs to
 CC treat diseases related to HOXD3 activity and in studying the effect of
 CC the variation on the biological activity of HOXD3 as well as on the
 CC binding affinity of candidate drugs targeting HOXD3 for the treatment of
 CC developmental disorders and tumours. An antibody against HOXD3 is useful
 CC in a variety of diagnostic and prognostic formats and therapeutic
 CC methods. A recombinant non-human organism is useful in studying
 CC expression of the HOXD3 isogenes in vivo. Allele-specific
 CC oligonucleotides (ASO) are useful as probes and primers and for assaying
 CC a polymorphism in the target region. The present sequence is a primer
 CC used for detecting human HOXD3 gene polymorphisms

XX SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12

DB 3 GGCGGCA 9

RESULT 632

ABN80657/c
 ID ABN80657 standard; DNA; 10 BP.

XX AC ABN80657;

DT 19-JUL-2002 (first entry)

XX Human P450(cytochrome) oxidoreductase ASO primer extension oligo #45.

XX Human; P450(cytochrome) oxidoreductase; POR; cancer; haplotype; SNP;
 KW single nucleotide polymorphism; flavoprotein; enzyme;
 KW primer extension oligonucleotide; ss.

XX OS Homo sapiens.

PN WO200226768-A2.

XX PD 04-APR-2002.

XX PF 01-OCT-2001; 2001WO-US030877.

XX PR 29-SEP-2000; 2000US-0236449P.

XX PA (GENA-) GENAISSANCE PHARM INC.

XX PI Kazemi A, Kliehm SE, Lanz EM, Messer C, Tanguay DA;

XX WPI; 2002-394236/42.

DR New genetic variants comprising haplotypes of the P450 (cytochrome)
 PT oxidoreductase (POR) isogene, useful in improving the efficiency of drug
 PT screening protocols for compounds targeting POR.

XX PS Claim 16; Page 15; 141pp; English.

XX The present invention provides the protein, gene and cDNA sequences of
 CC human P450(cytochrome) oxidoreductase POR, and single nucleotide
 CC polymorphisms (SNPs) identified therein. The sequences can be used to
 CC haplotype the POR gene of an individual, and to establish whether POR is
 CC a suitable target for drugs to treat cancer and disorders associated with
 CC impaired protein synthesis in cells. The present sequence is an allele
 CC specific primer extension oligonucleotide for the coding sequences of the
 CC invention

SQ Sequence 10 BP; 0 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12

DB 7 GGCGGCA 1

RESULT 633

ABV78532/c
 ID ABV78532 standard; CDNA; 10 BP.

XX AC ABV78532;

DT 29-NOV-2002 (first entry)

DE Human Th1 cell preferentially expressed EST SAGE tag, SEQ ID NO:243.

KW SAGE tag; serial analysis of gene expression; human; Th1 cell;
 KW activated T cell; T lymphocyte; immune response; expression pattern;
 KW preferential expression; immune disorder; EST; expressed sequence tag;
 KW ss.
 XX Homo sapiens.
 OS
 PN JP2002186482-A.
 XX
 PD 02-JUL-2002.
 XX
 XX
 PF 19-DEC-2000; 2000JP-00385816.
 XX
 PR 19-DEC-2000; 2000JP-00385816.
 XX
 PA (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 XX WPI; 2002-594261/64.
 DR
 XX Human activated Th1 and Th2 cell expression gene group, useful for the
 PT diagnosis and treatment of Th1 and Th2-related diseases.
 XX
 PS Claim 19; Page 12; 60pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are expressed in activated human Th1
 CC and/or Th2 cells. The SAGE tags of this invention consist of a sequence
 CC of 10 nucleotides located downstream of the 5'-CATG-3' sequence motif
 CC lying nearest to the polyA region of cDNAs derived from a variety of
 CC genes. These tags serve to uniquely identify each transcript and can thus
 CC be used to analyse the pattern of gene expression in particular cell
 CC types. The invention also relates to proteins encoded by the genes
 CC expressed in Th1 and/or Th2 cells, antibodies against these proteins, and
 CC inhibitors of the expression of groups of genes that are expressed in
 CC either or both the two cell types. Groups of genes expressed in Th1
 CC and/or Th2 cell types may be used for the diagnosis and treatment of Th1
 CC and Th2-related disorders. Sequences ABV78390-ABV78560 are SAGE tags
 CC representing 171 genes which are more highly expressed in Th1 cells
 CC compared with Th2 cells
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 CGGCATC 14
 DB 10 CGGCATC 4
 RESULT 634
 ABV84235/C
 ID ABV84235 standard; cDNA; 10 BP.
 AC
 AC ABV84235;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human chronic hepatitis C tissue overexpressed gene SAGE tag #45.
 XX
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002209591-A.
 XX
 PD 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 XX

PR 19-JAN-2001; 2001JP-00012328.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 DR WPI; 2002-631294/68.
 XX
 PT Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.
 XX
 PS Claim 1; Page 11; 139pp; Japanese.
 XX
 CC The invention relates to SAGE (serial analysis of gene expression) tags
 CC representing groups of genes which are differentially expressed in human
 CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced
 CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.
 CC The SAGE tags of this invention consist of a sequence of 10 nucleotides
 CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the
 CC polyA region of cDNAs derived from a variety of genes. These tags serve
 CC to uniquely identify each transcript and can thus be used to analyse the
 CC pattern of gene expression in particular cell types. The invention also
 CC relates to proteins encoded by the genes expressed in chronic hepatitis C
 CC liver tissue or HCC, antibodies against these proteins, and inhibitors of
 CC the expression of groups of genes that are overexpressed in chronic
 CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed
 CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and
 CC treatment of these diseases. Such genes, inhibitors of their expression
 CC or activity, and antibodies against the gene products may be used in the
 CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences
 CC ABV84191-ABV84290 are SAGE tags representing the 100 most highly
 CC expressed genes out of those genes which are overexpressed in chronic
 CC hepatitis C liver tissue compared with normal liver tissue
 XX
 SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGGCGGG 7
 DB 8 CGGCGGG 2
 RESULT 635
 ABV84447/C
 ID ABV84447 standard; cDNA; 10 BP.
 XX
 AC ABV84447;
 XX
 DT 12-DEC-2002 (first entry)
 XX
 DE Human HCC overexpressed gene SAGE tag #257.
 XX
 KW SAGE tag; serial analysis of gene expression; human; chronic hepatitis C;
 KW CH; liver tissue; hepatocellular carcinoma; cancer; tumour; HCC;
 KW expression pattern; differential expression; ss.
 XX
 OS Homo sapiens.
 XX
 PN JP2002209591-A.
 XX
 PD 30-JUL-2002.
 XX
 PF 19-JAN-2001; 2001JP-00012328.
 XX
 XX 19-JAN-2001; 2001JP-00012328.
 XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
 XX
 XX WPI; 2002-631294/68.
 DR Human chronic hepatitis C tissue expression exasperating gene group
 PT comprises 100 high-ranking genes.

XX Claim 19; Page 17; 139pp; Japanese.

PS The invention relates to SAGE (serial analysis of gene expression) tags

CC representing groups of genes which are differentially expressed in human

CC chronic hepatitis C (CH) liver tissue or hepatitis C-induced

CC hepatocellular carcinoma (HCC) compared with normal human liver tissue.

CC The SAGE tags of this invention consist of a sequence of 10 nucleotides

CC located downstream of the 5'-CATG-3' sequence motif lying nearest to the

CC polyA region of cDNAs derived from a variety of genes. These tags serve

CC to uniquely identify each transcript and can thus be used to analyse the

CC pattern of gene expression in particular cell types. The invention also

CC relates to proteins encoded by the genes expressed in chronic hepatitis C

CC liver tissue or HCC, antibodies against these proteins, and inhibitors of

CC the expression of groups of genes that are overexpressed in chronic

CC hepatitis C liver tissue or HCC. Groups of genes differentially expressed

CC in chronic hepatitis C tissue or HCC may be used for the diagnosis and

CC treatment of these diseases. Such genes, inhibitors of their expression

CC or activity, and antibodies against the gene products may be used in the

CC development of drugs to treat chronic hepatitis C and/or HCC. Sequences

CC ABV84391-ABV84490 are SAGE tags representing the 100 most highly

CC expressed genes out of those genes which are overexpressed in

CC hepatocellular carcinoma compared with normal liver tissue

XX SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGG 7

DB 8 CGCGGG 2

RESULT 636

ABK23563/C

ID ABK23563 standard; DNA; 10 BP.

XX AC ABK23563;

XX 09-APR-2002 (first entry)

XX Transcript tag DNA sequence #152 induced or suppressed by N-myc.

DE Myc-dependent downstream gene; neoplastic; cancer; growth; invasion;

XX spread; myc target; myc tag; SAGE; serial analysis of gene expression;

KW myc oncogene; N-myc; human neuroblastoma; cytostatic; ds.

XX OS Homo sapiens.

XX WO200185941-A2.

XX 15-NOV-2001.

XX 11-MAY-2001; 2001WO-NL000361.

XX 11-MAY-2000; 2000EP-00201698.

PR 29-JUN-2000; 2000EP-00202284.

XX (UYAM-) UNIV AMSTERDAM ACAD ZIEKENHUIS BLIJ VAN.

XX Versteeg R, Caron HN;

XX WPI; 2002-066603/09.

XX A new nucleic acid library of myc-dependent downstream genes capable of

PT supporting a neoplastic characteristic of cancer is useful to find new

PT therapies and diagnoses for cancer.

XX Disclosure; Page 53; 69pp; English.

XX The present invention relates to a nucleic acid library comprising myc-

CC dependent downstream genes or their functional fragments essentially

CC capable of supporting a neoplastic character of cancer such as growth,

CC invasion or spread. These myc target or tag sequences are identified by

CC SAGE (serial analysis of gene expression). The library is also useful to

CC new diagnoses and treatments for cancer. The invention is also useful to

CC enhance production of recombinant proteins in a production system with

CC high expression of endogenous or transfected myc oncogenes. ABK23412-

CC ABK23828 represent transcript tag DNA sequences that are activated or

XX repressed by N-myc in human neuroblastoma

XX SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14

DB 10 CGGCATC 4

RESULT 637

ABK81324

ID ABK81324 standard; DNA; 10 BP.

XX AC ABK81324;

XX 13-AUG-2002 (first entry)

DE Human ADMR gene allele-specific oligonucleotide PCR primer #21.

XX Human; G protein-coupled receptor similar to the adrenomedullin receptor;

KW ADMR; haplotyping; haplotype pair; congestive heart failure; primer; ss;

KW arterial hypertension; pulmonary hypertension; renal failure; sepsis;

KW chromosome 12; single nucleotide polymorphism; PCR.

XX OS Homo sapiens.

XX WO200226770-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-US030879.

XX 29-SEP-2000; 2000US-0236570P.

PR (GENA-) GENAISSANCE PHARM INC.

XX Choi JY, Lee HH, Shah N;

XX WPI; 2002-435192/46.

XX Novel G-protein coupled receptor similar to the adrenomedullin receptor

PT gene, useful therapeutically and in screening for drugs targeting

PT receptor polypeptide.

XX Claim 16; Page 14; 78pp; English.

XX The invention relates to single nucleotide polymorphisms in the gene

CC encoding the human G protein-coupled receptor similar to the

CC adrenomedullin receptor (ADMR) polypeptide. A method for haplotyping the

CC ADMR gene in an individual comprises identifying the nucleotide at one or

CC more polymorphic sites and determining whether one of the copies of the

CC gene is defined by one of the ADMR haplotypes given in the specification

CC or whether both copies are defined by a haplotype pair. This method is

CC useful in genotyping, whereby all possible haplotype pairs can be

CC assigned to specific genotypes. An association between a trait and a

CC haplotype or haplotype pair of the ADMR gene can be identified by

CC comparing the frequency of the haplotype or haplotype pair in a

CC population exhibiting the trait with the frequency of the haplotype or

CC haplotype pair in a reference population, where a higher haplotype

CC frequency in the trait population indicates the trait is associated with

CC the haplotype or haplotype pair. ADMR and its corresponding DNA are used

CC for studying the expression and function of ADMR, for use in screening
 CC for candidate drugs to treat diseases related to ADMR activity, such as
 CC congestive heart failure, arterial hypertension, pulmonary hypertension,
 CC renal failure, and sepsis. Sequences ABK81304-ABK81325 represent allele-
 CC specific oligonucleotide PCR primers used to detect ADMR gene
 CC polymorphisms
 XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 GCGCGGC 8
 |||||
 Db 1 GCGCGGC 7
 RESULT 638
 AAS95686
 ID AAS95686 standard; DNA; 10 BP.
 XX
 AC AAS95686;
 XX
 DT 14-FEB-2002 (first entry)
 XX
 DE Superoxide dismutase 1 (SOD1) allele-specific oligonucleotide #27.
 XX
 KW Superoxide dismutase 1; soluble amyotrophic lateral sclerosis 1 (adult);
 KW haplotyping; SOD1; allele-specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200185741-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 07-MAY-2001; 2001WO-US014772.
 XX
 PR 05-MAY-2000; 2000US-0202491P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 XX
 PI Choi JY, Bentivegna SC, Klem SE, Koshy B, Parks KE;
 XX WPI; 2002-055578/07.
 DR
 XX Isolated human superoxide dismutase 1 (SOD1) soluble polynucleotide,
 PT useful for screening therapeutic compounds, comprises a sequence which is
 PT a polymorphic variant of reference sequence for the SOD1 gene or its
 PT fragment.
 XX
 PS Claim 17; Page 13; 70pp; English.
 XX
 CC The invention relates to an isolated human superoxide dismutase 1,
 CC soluble (amyotrophic lateral sclerosis 1 (adult)) (SOD1) polynucleotide
 CC (I) comprising a sequence which is a polymorphic variant of a reference
 CC sequence for the SOD1 gene. Haplotyping the SOD1 gene of an individual,
 CC involves: (a) determining whether the individual has one of the SOD1
 CC haplotypes or haplotype pairs given in the specification; or (b)
 CC determining for one copy of the SOD1 gene present in the individual, the
 CC identity of the nucleotide at two or more polymorphic sites selected from
 CC PSI-7. The method is useful for determining whether an individual has a
 CC haplotype or haplotype pairs defined in the specification. The method is
 CC also useful for improving the efficacy and reliability of several steps
 CC in the discovery and development of drugs for treating diseases
 CC associated with SOD1 activity, e.g., amyotrophic lateral sclerosis, and
 CC to validate SOD1 as a candidate agent for treating a specific condition
 CC or disease associated with SOD1 activity. It can further be used in the
 CC design of clinical trials of candidate drugs for treating a specific
 CC condition or disease predicted to be associated with SOD1 activity. (I)
 CC is useful in studying the expression and function of SOD1, and in
 CC expressing SOD1 protein for use in screening for candidate drugs to treat

CC diseases related to SOD1 activity. AAS95660-AAS95710 represent human
 CC superoxide dismutase 1, soluble (amyotrophic lateral sclerosis 1 (adult))
 CC (SOD1) allele-specific oligonucleotides and related PCR primers as
 CC described in the method of the invention
 XX
 SQ Sequence 10 BP; 1 A; 4 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GCGCGGC 11
 |||||
 Db 2 GCGCGGC 8
 RESULT 639
 ABA93354
 ID ABA93354 standard; DNA; 10 BP.
 XX
 AC ABA93354;
 XX
 DT 22-APR-2002 (first entry)
 XX
 DE Human ACAA1 gene polymorphism detection primer SEQ ID NO:69.
 XX
 KW Human; acetyl-Coenzyme A acyltransferase; ACAA1; chromosome 3p23-p22;
 KW peroxisomal 3-oxoacyl-Coenzyme A thiolase; SNP; genotype; haplotype;
 KW single nucleotide polymorphism; polymorphic variant; enzyme; probe;
 KW primer; allele specific oligonucleotide; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200187903-A2.
 XX
 PD 22-NOV-2001.
 XX
 PF 03-MAY-2001; 2001WO-US014330.
 XX
 PR 18-MAY-2000; 2000US-0205022P.
 XX
 PA (GENA-) GENAISSANCE PHARM INC.
 PA (DUDA/) DUDA A E.
 XX
 PI Chew A, Koshy B;
 XX WPI; 2002-164134/21.
 DR
 XX Isolated polynucleotide, comprising a polymorphic variant of the acetyl-
 PT Coenzyme A acyltransferase 1 (peroxisomal 3-oxoacyl-Coenzyme A thiolase)
 PT gene useful for providing haplotype information and in therapy for
 PT treating related disorders.
 XX
 PS Claim 17; Page 14; 93pp; English.
 XX
 CC The present invention describes a polypeptide (I) which is a polymorphic
 CC variant (PV) of the acetyl-Coenzyme A acyltransferase (peroxisomal 3-
 CC oxoacyl-Coenzyme A thiolase) ACAA1 protein (AB055516). ACAA1 is located
 CC on chromosome 3p23-p22. (I) can be encoded by ABA93286 (or ABA93288)
 CC where the sequence comprises one of the haplotypes shown in Table 4 or
 CC one of the haplotype pairs shown in Table 3, where Tables 3 and 4 are
 CC given in the specification. The polynucleotide encoding ACAA1 can be used
 CC for providing haplotype and genotype information of an individual.
 CC Furthermore, the polynucleotide is useful for the treatment of disorders
 CC related to its abnormal expression or function. ABA93289 to ABA93383
 CC represent allele specific oligonucleotides (ASOs) which are used in the
 CC detection of polymorphisms in the human ACAA1 gene
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 GGGCGGC 11
Db      1 GGGCGGC 7

RESULT 640
AAD26959
ID  AAD26959 standard; DNA; 10 BP.
XX
AC  AAD26959;
XX
XX  09-APR-2002 (first entry)
XX
XX  Oligonucleotide used to isolate hITF probe by PCR.
XX
XX  Intestinal trefoil factor; ITF; inflammatory bowel disease; therapy;
KW  bacterial infection; peptic ulcer; radiation surgery; antiulcer;
KW  antiinflammatory; ss.
XX
OS  Unidentified.
XX
XX  US6316218-B1.
XX
XX  13-NOV-2001.
XX
XX  27-JAN-1998; 98US-00056868.
XX
XX  14-FEB-1991; 91US-00655965.
XX  13-FEB-1992; 92US-00837192.
XX  25-MAR-1993; 93US-00037741.
XX  02-FEB-1994; 94US-00191352.
XX
PA  (GEO ) GEN HOSPITAL CORP.
XX
XX  Podolsky DK;
XX
XX  WPI; 2002-121020/16.
XX
XX  A nucleic acid encoding an intestinal trefoil factor is useful to treat
PT  peptic ulcers and inflammatory bowel disease, and to protect the
PT  intestine against injury from insults such as bacterial infection and
PT  radiation surgery.
XX
PS  Disclosure; Col 7; 17pp; English.
XX
XX  The present invention relates to an isolated nucleic acid that encodes an
CC  intestinal trefoil factor (ITF) polypeptide. The intestinal trefoil
CC  factor can be used to treat peptic ulcers and inflammatory bowel diseases
CC  and to protect the intestinal tract from injury caused by bacterial
CC  infection, radiation surgery or other insults. It may also be used to
CC  protect and stabilise other proteins in the digestive tract. The present
CC  sequence is an oligonucleotide used in the isolation of human ITF (hITF)
CC  probe by PCR
XX
SQ  Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match 43.8%; Score 7; DB 1; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY      5 GGGCGGC 11
Db      1 GGGCGGC 7

RESULT 641
AAD44209
ID  AAD44209 standard; cDNA; 10 BP.
XX
AC  AAD44209;
XX
XX  13-DEC-2002 (first entry)
XX

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XX  Human TANGO 239 form 1 cDNA 3' end fragment.
DE
XX  TANGO protein; vaccine; chromosomal mapping; antisense gene therapy;
KW  forensic biology; predictive medicine; cytostatic; pharmacogenomic;
KW  tissue typing; human; ss.
XX
OS  Homo sapiens.
XX
XX  US200205139-A1.
XX
XX  09-MAY-2002.
XX
XX  01-MAR-2001; 2001US-00796858.
XX
XX  30-DEC-1998; 98US-00223094.
XX  30-DEC-1998; 98US-00223546.
XX  30-DEC-1998; 98US-00224246.
XX  14-MAY-1999; 99US-00312359.
XX  18-JUN-1999; 99US-00336536.
XX  29-JUN-1999; 99US-00342687.
XX  30-JUL-1999; 99US-00365164.
XX  20-SEP-1999; 99US-00399723.
XX  23-DEC-1999; 99US-00471179.
XX  29-DEC-1999; 99US-00474071.
XX  29-DEC-1999; 99US-00474072.
XX  15-MAY-2000; 2000US-00572002.
XX  19-JUN-2000; 2000US-00597993.
XX  22-JUN-2000; 2000US-00599596.
XX  29-JUN-2000; 2000US-00606565.
XX  31-JUN-2000; 2000US-00630334.
XX  20-SEP-2000; 2000US-00665666.
XX
XX  (HOLT/) HOLTZMAN D A.
PA  (SHAR/) SHARP J D.
PA  (LEIB/) LEIBY K R.
PA  (BOSS/) BOSSONE S.
PA  (PANY/) PAN Y.
PA  (BARN/) BARNES T M.
PA  (FRAS/) FRASER C C.
PA  (WRIG/) WRIGHTON N.
PA  (MYER/) MYERS P S.
PA  (KING/) KINGSBURY G.
XX
XX  Holtzman DA, Sharp JD, Leiby KR, Bossone S, Pan Y, Barnes TM;
XX  Fraser CC, Wrighton N, Myers PS, Kingsbury G;
XX  WPI; 2002-453953/48.
XX
XX  New isolated nucleic acid encoding a TANGO polypeptide, for use as a
PT  modulating agent for regulating cellular processes and for use in a
PT  vaccine.
XX
XX  Disclosure; Page 12; 206pp; English.
XX
XX  The invention relates to TANGO polypeptide and its corresponding nucleic
CC  acid sequence. TANGO protein is used to identify a compound which binds
CC  to it that can be used for modulating its activity. It is also used to
CC  produce an antibody. The antibody is used to detect the presence of the
CC  polypeptide in a sample. TANGO DNA and protein are useful as modulating
CC  agents in regulating cellular processes. They can be used in vaccines.
CC  TANGO DNA and protein and its antibody are used in e.g. chromosomal
CC  mapping, tissue typing, forensic biology, predictive medicine,
CC  pharmacogenomics and treatment methods. TANGO DNA is used in antisense
CC  gene therapy. The present sequence is human TANGO 239 form 1 cDNA
XX  fragment
XX
XX  Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
XX
XX  Query Match 43.8%; Score 7; DB 1; Length 10;
XX  Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX  Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      5 GGGCGGC 11
DB      1 GGGCGGC 7

RESULT 642
AAD32318
ID  AAD32318 standard; DNA; 10 BP.
XX
AC  AAD32318;
DT      18-JUN-2002 (first entry)
XX
DE  Human neurotrophin 3 (NTF3) gene polymorphism detecting primer #4.
XX
KW  Human; genetic variant; neurotrophin 3; NTF3; haplotyping; genotyping;
KW  nervous system disorder; congenital heart defect; gene therapy;
KW  therapeutic; polymorphism; primer; ss.
XX
OS  Homo sapiens.
XX
PN  WO200212499-A2.
XX
PD  14-FEB-2002.
XX
PF  06-AUG-2001; 2001WO-US024665.
XX
PR  04-AUG-2000; 2000US-0223208P.
XX
PA  (GENA-) GENAISSANCE PHARM INC.
XX
PI  Kliem SE, Koshy B, Lanz EM;
XX
DR  WPI; 2002-269092/31.
XX
PT  Novel polymorphic variants of neurotrophin 3 (NTF3), useful for studying
PT  the expression and function of NTF3, and for screening candidate drugs to
PT  treat nervous system disorders and congenital heart defects.
XX
PS  Claim 19; Page 13; 60pp; English.
XX
CC  The present invention relates to genetic variants of human neurotrophin
CC  (NTF) 3 gene. The invention also relates to compositions and methods for
CC  haplotyping and/or genotyping the NTF3 gene in an individual. Sequences
CC  of the invention are useful for studying the expression and function of
CC  NTF3 protein for use in screening for candidate drugs to treat diseases
CC  related to NTF3 activity. The polymorphism and haplotype data is useful
CC  for validating whether NTF3 is a suitable target for drugs to treat
CC  nervous system disorders and congenital heart defects, screening for such
CC  drugs and reducing bias in clinical trials of such drugs. They are also
CC  useful for therapeutic purposes. The haplotyping method is useful for
CC  improving the efficiency and outcome of several steps in the discovery
CC  and development of drugs for treating diseases associated with NTF3
CC  activity such as nervous system disorders and congenital heart defects.
CC  It is also useful for validating NTF3 as a candidate target for treating
CC  a specific condition or disease predicted to be associated with NTF3
CC  activity. The method is also useful for screening compounds to treat a
CC  specific condition or disease predicted to be associated with NTF3
CC  activity. Sequences of the invention are also used in gene therapy. The
CC  present DNA sequence is a primer used to detect human NTF3 gene
CC  polymorphisms
XX
SQ  Sequence 10 BP; 0 A; 3 C; 5 G; 2 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GGGCGGC 8
DB      4 GGGCGGC 10

RESULT 643
ABK93089
ID  ABK93089 standard; DNA; 10 BP.
XX
AC  ABK93089;
DT      22-AUG-2002 (first entry)
XX
DE  Human cancer related gene associated primer #1.
XX
KW  Human; cancer; DNA array; gene expression analysis; primer; PCR; ss.
XX
OS  Homo sapiens.
XX
PN  JP2002058495-A.
XX
PD  26-FEB-2002.
XX
PF  22-AUG-2000; 2000JP-00255737.
XX
PR  22-AUG-2000; 2000JP-00255737.
XX
PA  (HITA ) HITACHI LTD.
XX
DR  WPI; 2002-398777/43.
XX
PT  A DNA array that observes the expression of cancer related genes is
PT  useful for the elucidation of the action mechanism of anticancer agents.
XX
PS  Disclosure; Page 8; 71pp; Japanese.
XX
CC  The invention relates to a DNA array for identifying cancer related
CC  genes. The DNA array comprises: (a) statistically significantly higher
CC  results of over 10% in homology search of a DNA molecule describing
CC  different genes or a complementary DNA (GDNA); (b) statistically
CC  significantly higher results (p value) of over 10% in homology search
CC  with human Alu sequence; (c) difference of melting temperature of the DNA
CC  fragment and hybridisation temperature at 30 degree C or less; (d) the
CC  DNA fragment prepared by immobilisation of a DNA short sequence with a
CC  specific higher order structure; and (e) the DNA fragment without short
CC  repetitive sequence. The array is used in elucidation of the action
CC  mechanism of anticancer agents. ABK92989-ABK93090 represent human cancer
CC  related genes and associated primers of the invention
XX
SQ  Sequence 10 BP; 0 A; 2 C; 8 G; 0 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGGCGGC 11
DB      1 GGGCGGC 7

RESULT 644
AAS99398
ID  AAS99398 standard; DNA; 10 BP.
XX
AC  AAS99398;
XX
DT      12-MAR-2002 (first entry)
XX
DE  Aldehyde dehydrogenase 5 family, member A1, oligonucleotide #91.
XX
KW  Aldehyde dehydrogenase 5 family member A1; ALDH5A1;
KW  succinate-semialdehyde dehydrogenase; gene therapy; primer;
KW  antisense technology; primer extension oligonucleotide;
KW  4-hydroxybutyric aciduria; metabolic disease; transgenic animal; ss.
XX
OS  Synthetic.
XX
PN  WO200190119-A2.

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XX PD 29-NOV-2001.
XX PF 21-MAY-2001; 2001WO-US016558.
XX PR 19-MAY-2000; 2000US-0205849P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Klien SE, Koshi B, Tanguay DA;
XX DR WPI; 2002-089912/12.
XX PT New genetic variants of human aldehyde dehydrogenase 5 family, member A1,
PT ALDH5A1 gene for treating metabolic diseases and for expressing ALDH5A1
PT protein useful in identifying drugs to treat 4-hydroxybutyric aciduria.
XX PS Claim 18; Page 14; 151pp; English.
XX CC The invention describes an isolated polynucleotide comprising a
CC nucleotide sequence which is a polymorphic variant of a reference
CC sequence for the aldehyde dehydrogenase 5 family, member A1 (succinate-
CC semialdehyde dehydrogenase) (ALDH5A1) gene or its fragment. The
CC polypeptide is useful for screening for drugs targeting it by contacting
CC the ALDH5A1 polymorphic variant with a candidate agent and assaying for
CC binding activity. The polypeptide and haplotypes are useful for
CC identifying an association between a trait such as a clinical response to
CC a drug targeting ALDH5A1 and a haplotype ALDH5A1 gene. Transgenic animals
CC are also useful for studying expression of the ALDH5A1 isogenes in vivo,
CC for in vivo screening and testing of drugs against ALDH5A1 protein and
CC for testing the efficacy of therapeutic agents and compounds for 4-
CC hydroxybutyric aciduria and metabolic diseases in a biological system.
CC Antibodies are useful for diagnostic and prognostic formats and
CC therapeutic methods, for immunoprecipitating the polypeptide from
CC solution, for detecting ALDH5A1 protein isoforms in biological samples,
CC frozen tissue sections, for use in immunocytochemical,
CC immunohistochemical and immunofluorescence techniques. The polynucleotide
CC is useful for gene therapy and antisense gene therapy. This sequence is a
CC primer extension oligonucleotide used to detect polymorphisms in the
CC ALDH5A1 gene described in the method of the invention
XX SQ Sequence 10 BP; 2 A; 2 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GCGCGCA 12
DB 3 GCGCGCA 9

RESULT 645
AAD26797/c
ID AAD26797 standard; DNA; 10 BP.
XX AC AAD26797;
XX OS Homo sapiens.
XX PN WO200190126-A2.
XX PD 29-NOV-2001.
XX PF 23-MAY-2001; 2001WO-US016938.

Primer #4 to detect human SNAP29 gene polymorphisms.
Human; synaptosomal-associated protein 29 kD; SNAP29 protein;
haplotyping; genotyping; membrane trafficking related disorder;
gene therapy; polymorphism; primer; ss.
Homo sapiens.
WO200190126-A2.
29-NOV-2001.
23-MAY-2001; 2001WO-US016938.

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XX PR 23-MAY-2000; 2000US-0206529P.
XX PA (GENA-) GENAISSANCE PHARM INC.
XX PI Kazemi A, Koshi B, Tanguay DA;
XX DR WPI; 2002-089916/12.
XX PT Novel isolated polynucleotide, a polymorphic variant of synaptosomal-
PT associated protein, 29 kD (SNAP29) gene useful for expressing SNAP29
PT protein isoform to screen drugs to treat SNAP29 activity-related disease.
XX PS Claim 18; Page 14; 115pp; English.
XX CC The invention relates to genetic variants of human synaptosomal-
CC associated protein, 29 kD (SNAP29) gene. The invention also relates to
CC compositions and methods for haplotyping and/or genotyping the SNAP29
CC gene in an individual. Polynucleotides of the invention are useful for
CC studying the expression and function of SNAP29 and expressing SNAP29
CC protein for use in screening candidate drugs to treat diseases related to
CC SNAP29 activity. They are also used in gene therapy. The genotyping
CC method is useful for determining if an individual has one of haplotype or
CC haplotype pairs. The polymorphism and haplotype data is useful for
CC validating whether SNAP29 is a suitable target for drugs to treat
CC disorders related to membrane trafficking, screening for such drugs and
CC reducing bias cells in clinical trials of such drugs. The present
CC sequence is a primer for detecting human SNAP29 gene polymorphisms
XX SQ Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GCGCGCA 12
DB 7 GCGCGCA 1

RESULT 646
ADG28269
ID ADG28269 standard; DNA; 10 BP.
XX AC ADG28269;
XX DT 26-FEB-2004 (first entry)
XX DE Human Myo/V1 protein-related Nf-kappaB regulation site SeqID344.
XX KW cardiac-associated protein; Myo/V1 protein; MP; cardiac; vasotropic;
KW immunosuppressive; vulnery; Nf-kappaB p50; Nf-kappaB p65;
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;
KW ischaemia; reperfusion injury; heart transplantation;
KW anti-ageing treatment; human; ds.
XX OS Homo sapiens.
XX PN WO200245659-A2.
XX PD 13-JUN-2002.
XX PF 26-OCT-2001; 2001WO-US051272.
XX PR 27-OCT-2000; 2000US-0243985P.
XX PA (BAYU ) BAYLOR COLLEGE MEDICINE.
XX PI Sivasubramanian N, Knuefermann P, Mann DL;
XX DR WPI; 2002-537532/57.
XX PT Novel dominant negative mutant sequence or constitutively active mutant

```

PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
PT disorders and inhibiting formation of NFkappaB homodimers.
XX
XX Claim 45; SEQ ID NO 344; 217pp; English.
XX
XX This invention relates to a novel dominant negative or constitutively
CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
CC invention may be useful for the development of compounds with a cardiant,
CC vasotropic, immunosuppressive or vulnerary activity through the
CC inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
CC invention may be useful for the development of treatments for
CC cardiovascular disease including cardiac hypertrophy, myocardial
CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
CC mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
CC p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
CC reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX
XX Sequence 10 BP; 0 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGC 8
DB 1 GCGGGC 7
RESULT 647
ADG28255
ID ADG28255 standard; DNA; 10 BP.
AC
AC ADG28255;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human Myo/VI protein-related NFkappaB regulation site SeqID330.
DE
XX cardiac-associated protein; Myo/VI protein; MP; cardiant; vasotropic;
KW immunosuppressive; vulnerary; NFkappaB p50; NFkappaB p65;
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;
KW ischaemia; reperfusion injury; heart transplantation;
KW anti-ageing treatment; human; ds.
XX
XX Homo sapiens.
XX
XX WO200245659-A2.
XX
XX 13-JUN-2002.
XX
XX 26-OCT-2001; 2001WO-US051272.
XX
XX 27-OCT-2000; 2000US-0243985P.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Sivasubramanian N, Knuefermann P, Mann DL;
XX
XX WPI; 2002-537532/57.
XX
XX Novel dominant negative mutant sequence or constitutively active mutant
PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
PT disorders and inhibiting formation of NFkappaB homodimers.
XX
XX Claim 45; SEQ ID NO 330; 217pp; English.
XX
XX This invention relates to a novel dominant negative or constitutively
CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
CC invention may be useful for the development of compounds with a cardiant,
CC vasotropic, immunosuppressive or vulnerary activity through the
CC inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
CC invention may be useful for the development of treatments for
CC cardiovascular disease including cardiac hypertrophy, myocardial

CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
CC mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
CC p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
CC reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX
XX Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 GCGGGC 11
DB 2 GCGGGC 8
RESULT 648
ADG28205
ID ADG28205 standard; DNA; 10 BP.
XX
AC ADG28205;
XX
XX 26-FEB-2004 (first entry)
XX
XX Human Myo/VI protein-related NFkappaB regulation site SeqID280.
DE
XX cardiac-associated protein; Myo/VI protein; MP; cardiant; vasotropic;
KW immunosuppressive; vulnerary; NFkappaB p50; NFkappaB p65;
KW cardiovascular disease; cardiac hypertrophy; myocardial infarction;
KW ischaemia; reperfusion injury; heart transplantation;
KW anti-ageing treatment; human; ds.
XX
XX Homo sapiens.
XX
XX WO200245659-A2.
XX
XX 13-JUN-2002.
XX
XX 26-OCT-2001; 2001WO-US051272.
XX
XX 27-OCT-2000; 2000US-0243985P.
XX
XX (BAYU) BAYLOR COLLEGE MEDICINE.
XX
XX Sivasubramanian N, Knuefermann P, Mann DL;
XX
XX WPI; 2002-537532/57.
XX
XX Novel dominant negative mutant sequence or constitutively active mutant
PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
PT disorders and inhibiting formation of NFkappaB homodimers.
XX
XX Claim 45; SEQ ID NO 280; 217pp; English.
XX
XX This invention relates to a novel dominant negative or constitutively
CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
CC invention may be useful for the development of compounds with a cardiant,
CC vasotropic, immunosuppressive or vulnerary activity through the
CC inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
CC invention may be useful for the development of treatments for
CC cardiovascular disease including cardiac hypertrophy, myocardial
CC infarction, ischaemia/reperfusion injury and heart transplantation, in a
CC mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
CC p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
CC reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX
XX Sequence 10 BP; 0 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGC 8

```

Db          1 GCGCGGC 7
          |||||
RESULT 649
ADG28054
ID  ADG28054 standard; DNA; 10 BP.
XX
XX  AC  ADG28054;
XX  DT  26-FEB-2004 (first entry)
XX  DE  Human Myo/V1 protein-related NFkappaB regulation site SeqID23.
XX  KW  cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic;
XX  KW  immunosuppressive; vulnery; NFkappaB p50; NFkappaB p65;
XX  KW  cardiovascular disease; cardiac hypertrophy; myocardial infarction;
XX  KW  ischaemia; reperfusion injury; heart transplantation;
XX  KW  anti-ageing treatment; human; ds.
XX  OS  Homo sapiens.
XX  PN  WO200245659-A2.
XX  PD  13-JUN-2002.
XX  PF  26-OCT-2001; 2001WO-US051272.
XX  PR  27-OCT-2000; 2000US-0243985P.
XX  PS  Claim 45; SEQ ID NO 23; 217pp; English.
XX  PA  (BAYU ) BAYLOR COLLEGE MEDICINE.
XX  PI  Sivasubramanian N, Knuefermann P, Mann DL;
XX  DR  WPI; 2002-537532/57.
XX  PT  Novel dominant negative mutant sequence or constitutively active mutant
XX  PT  sequence of Myo/V1 polypeptide, useful for treating cardiovascular
XX  PT  disorders and inhibiting formation of NFkappaB homodimers.
XX  PS  Claim 45; SEQ ID NO 23; 217pp; English.
XX  CC  This invention relates to a novel dominant negative or constitutively
XX  CC  active mutant sequence of the cardiac-associated Myo/V1 protein (MP). The
XX  CC  invention may be useful for the development of compounds with a cardiant,
XX  CC  vasotropic, immunosuppressive or vulnerary activity through the
XX  CC  inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
XX  CC  invention may be useful for the development of treatments for
XX  CC  cardiovascular disease including cardiac hypertrophy, myocardial
XX  CC  infarction, ischaemia/reperfusion injury and heart transplantation, in a
XX  CC  mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
XX  CC  p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
XX  CC  reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX  SQ  Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCGGC 11
        |||||
Db      2 GCGCGGC 8

RESULT 650
ADG28258
ID  ADG28258 standard; DNA; 10 BP.
XX
XX  AC  ADG28258;
XX  DT  26-FEB-2004 (first entry)
XX

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DE  Human Myo/V1 protein-related NFkappaB regulation site SeqID333.
XX
XX  KW  cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic;
XX  KW  immunosuppressive; vulnery; NFkappaB p50; NFkappaB p65;
XX  KW  cardiovascular disease; cardiac hypertrophy; myocardial infarction;
XX  KW  ischaemia; reperfusion injury; heart transplantation;
XX  KW  anti-ageing treatment; human; ds.
XX  OS  Homo sapiens.
XX  PN  WO200245659-A2.
XX  PD  13-JUN-2002.
XX  PF  26-OCT-2001; 2001WO-US051272.
XX  PR  27-OCT-2000; 2000US-0243985P.
XX  PS  Claim 45; SEQ ID NO 333; 217pp; English.
XX  PA  (BAYU ) BAYLOR COLLEGE MEDICINE.
XX  PI  Sivasubramanian N, Knuefermann P, Mann DL;
XX  DR  WPI; 2002-537532/57.
XX  PT  Novel dominant negative mutant sequence or constitutively active mutant
XX  PT  sequence of Myo/V1 polypeptide, useful for treating cardiovascular
XX  PT  disorders and inhibiting formation of NFkappaB homodimers.
XX  PS  Claim 45; SEQ ID NO 333; 217pp; English.
XX  CC  This invention relates to a novel dominant negative or constitutively
XX  CC  active mutant sequence of the cardiac-associated Myo/V1 protein (MP). The
XX  CC  invention may be useful for the development of compounds with a cardiant,
XX  CC  vasotropic, immunosuppressive or vulnerary activity through the
XX  CC  inhibition of formation of NFkappaB p50 or NFkappaB p65 homodimers. The
XX  CC  invention may be useful for the development of treatments for
XX  CC  cardiovascular disease including cardiac hypertrophy, myocardial
XX  CC  infarction, ischaemia/reperfusion injury and heart transplantation, in a
XX  CC  mammal, for anti-ageing treatment, for inhibiting formation of NFkappaB
XX  CC  p50 homodimers or NFkappaB p65 homodimers in a cell of a mammal and for
XX  CC  reducing formation of NFkappaB p65 homodimers in a cell of a mammal.
XX  SQ  Sequence 10 BP; 0 A; 5 C; 5 G; 0 T; 0 U; 0 Other;

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches      7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCGGC 11
        |||||
Db      1 GCGCGGC 7

RESULT 651
ADG28065
ID  ADG28065 standard; DNA; 10 BP.
XX
XX  AC  ADG28065;
XX  DT  26-FEB-2004 (first entry)
XX  DE  Human Myo/V1 protein-related NFkappaB regulation site SeqID34.
XX  KW  cardiac-associated protein; Myo/V1 protein; MP; cardiant; vasotropic;
XX  KW  immunosuppressive; vulnery; NFkappaB p50; NFkappaB p65;
XX  KW  cardiovascular disease; cardiac hypertrophy; myocardial infarction;
XX  KW  ischaemia; reperfusion injury; heart transplantation;
XX  KW  anti-ageing treatment; human; ds.
XX  OS  Homo sapiens.
XX  PN  WO200245659-A2.
XX

```

PD 13-JUN-2002.
 XX
 PF 26-OCT-2001; 2001WO-US051272.
 XX
 PR 27-OCT-2000; 2000US-0243985P.
 XX
 PA (BAYU) BAYLOR COLLEGE MEDICINE.
 XX
 PI Sivasubramanian N, Knuefermann P, Mann DL;
 XX WPI; 2002-537532/57.
 XX
 XX Novel dominant negative mutant sequence or constitutively active mutant
 PT sequence of Myo/VI polypeptide, useful for treating cardiovascular
 PT disorders and inhibiting formation of NfkappaB homodimers.
 XX
 PS Claim 45; SEQ ID NO 34; 217pp; English.
 XX
 XX This invention relates to a novel dominant negative or constitutively
 CC active mutant sequence of the cardiac-associated Myo/VI protein (MP). The
 CC invention may be useful for the development of compounds with a cardiant,
 CC vasotropic, immunosuppressive or vulnerary activity through the
 CC inhibition of formation of NfkappaB p50 or NfkappaB p65 homodimers. The
 CC invention may be useful for the development of treatments for
 CC cardiovascular disease including cardiac hypertrophy, myocardial
 CC infarction, ischemia/reperfusion injury and heart transplantation, in a
 CC mammal, for anti-ageing treatment, for inhibiting formation of NfkappaB
 CC p50 homodimers or NfkappaB p65 homodimers in a cell of a mammal and for
 CC reducing formation of NfkappaB p65 homodimers in a cell of a mammal.
 XX
 SQ Sequence 10 BP; 0 A; 5 C; 5 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCGGC 11
 Db 1 GGGCGGC 7
 RESULT 652
 ABZ80704
 ID ABZ80704 standard; DNA; 10 BP.
 XX
 AC ABZ80704;
 XX
 DT 07-JUL-2003 (first entry)
 XX
 DE UME6 consensus binding sequence #2.
 XX
 XX binding sequence; ss; UME6; meiosis; transcriptional regulation; MEME;
 KW gene network; quantitative disruptant data library; gene expression;
 KW gene regulation; Multiple Expectation-Maximization for motif Elicitation;
 KW Consensus.
 XX
 OS Homo sapiens.
 XX
 XX WO2003027262-A2.
 PN
 XX
 PD 03-APR-2003.
 XX
 XX 26-SEP-2002; 2002WO-US031093.
 PF
 XX 26-SEP-2001; 2001US-0325016P.
 PR 29-NOV-2001; 2001US-0334230P.
 PR 29-NOV-2001; 2001US-0334255P.
 PR 29-NOV-2001; 2001US-0334372P.
 PR 08-APR-2002; 2002US-0370824P.
 PR 19-JUL-2002; 2002US-0397458P.
 XX
 XX (GENE-) GENE/NETWORKS INC.
 PA
 XX

PI Imoto S, Goto T, Miyano S, Tashiro K, De Hoon M, Savoie CJ;
 PI Kuhara S;
 XX WPI; 2003-371918/35.
 DR
 XX
 PT Gene network construction, involves creating gene expression matrix based
 PT on expression result of gene disruption, using Bayesian computational
 PT model such that BNRC criterion is minimum.
 XX
 XX Disclosure; Page 11; 161pp; English.
 XX
 CC The invention relates to a method of constructing gene networks by
 CC providing a quantitative disruptant data library for a set of genes of an
 CC organism, including expression results of disruption of each gene,
 CC quantifying average effect and variability measure of each disruption for
 CC every other gene, creating gene expression matrix, generating network of
 CC relationship between genes, and determining differential expression of
 CC gene groups. The method is useful for constructing gene network for genes
 CC of organism to predict putative therapeutic targets. The method provides
 CC internal control and quantitative measurement of the direct effects of
 CC the presence or absence of the gene on the expression of other genes.
 CC Therefore selection of disruptant experiments to maximize the elucidation
 CC of gene control relationships is achieved to generate useful gene
 CC regulatory information. To illustrate the invention, Multiple Expectation
 CC -Maximization for motif Elicitation (MEME) was performed on 34 genes
 CC controlled by UME6, a global transcriptional regulator of meiotic genes.
 CC This consensus sequence was found in 32.4% of genes examined. This
 CC sequence is defined as the binding site for a repressor of the CAR1 gene
 XX
 SQ Sequence 10 BP; 1 A; 2 C; 5 G; 2 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02; Indels 0; Gaps 0;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCGGC 11
 Db 2 GGGCGGC 8
 RESULT 653
 ACC41654
 ID ACC41654 standard; DNA; 10 BP.
 XX
 AC ACC41654;
 XX
 DT 21-MAY-2003 (first entry)
 XX
 DE Zinc finger protein DNA-binding domain target sequence SEQ ID NO:201.
 XX
 KW Zinc finger domain; zinc finger; zinc finger binding domain; probe;
 KW chimeric nucleic acid; library; PCR primer; ss.
 XX
 OS Synthetic.
 XX
 XX WO2003016571-A1.
 PN
 XX
 PD 27-FEB-2003.
 XX
 XX 17-AUG-2002; 2002WO-KR001560.
 PF
 PR 17-AUG-2001; 2001US-0313402P.
 PR 22-APR-2002; 2002US-0374355P.
 XX
 XX (TOOL-) TOOLGEN INC.
 PA
 XX Kim J, Bae K, Park K, Kwon Y, Ryu E, Hwang M;
 PI WPI; 2003-268344/26.
 DR
 XX New library comprising polypeptides having zinc finger domains, useful
 PT for producing chimeric nucleic acids.
 XX

PS Claim 40; Page 101; 234pp; English.

XX The present invention describes a library comprising polypeptides. Each

CC polypeptide comprises a first or second zinc finger domain. The domains

CC of each polypeptide are identical to a zinc finger domain from a

CC naturally occurring protein and either do not occur in the same naturally

CC occurring protein or occur in the same naturally occurring protein in a

CC different configuration than in the polypeptide. The domains vary among

CC polypeptides. Also described: (1) producing chimeric nucleic acids; (2)

CC generating an artificial zinc finger polypeptide that specifically binds

CC to a target DNA site; and (3) identifying a nucleic acid encoding a zinc

CC finger polypeptide that specifically recognises a target DNA site. The

CC library can be used for producing chimeric nucleic acids. ACC41551 to

CC ACC41758 and ABR40919 to ABR41015 represent nucleotide and amino acid

CC sequences given in the exemplification of the present invention

XX

SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGG 7

Db 2 CGGCGGG 8

|||||

RESULT 654

ABT14274

ID ABT14274 standard; DNA; 10 BP.

XX

AC ABT14274;

XX

DT 20-FEB-2003 (first entry)

XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #44.

XX

XX Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;

KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX

OS Unidentified.

XX

PN WO200281743-A2.

XX

PD 17-OCT-2002.

XX

XX

PF 28-MAR-2002; 2002WO-GB001489.

XX

PR 02-APR-2001; 2001GB-00008182.

XX

XX (HAMI/) HAMILL B.

PA

PI Hamill B;

XX

XX WPI; 2003-075484/07.

XX

PT Amplification of nucleotide sequences from polynucleotides by chain

PT extension of oligonucleotide primers, comprises 2 oligonucleotides in

PT solution, 2 attached to supports and both share complementary sequences.

XX

PS Disclosure; Fig 17; 60pp; English.

XX

XX The invention comprises a method for the PCR amplification of nucleic

CC acids. The method involves a set of primers, where two of the primers are

CC in solution and at least two other primers are attached to a solid

CC support. The method of the invention can be used for the analysis of a

CC nucleic acid or a mixture of nucleic acids, including: single-stranded

CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The

CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)

CC PCR primer of the invention

XX

SQ Sequence 10 BP; 1 A; 3 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13

Db 8 GCGGCAT 2

|||||

RESULT 656

ACA62091

ID ACA62091 standard; DNA; 10 BP.

XX

AC ACA62091;

XX

DT 19-AUG-2003 (first entry)

XX

DE Gustductin alpha subunit cloning associated adaptor #2.

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 GGCATCG 15

Db 1 GGCATCG 7

|||||

RESULT 655

ABT14362/c

ID ABT14362 standard; DNA; 10 BP.

XX

AC ABT14362;

XX

DT 20-FEB-2003 (first entry)

XX

DE Nucleic acid PCR amplification method-related RAPD PCR primer #132.

XX

XX Nucleic acid amplification; nucleic acid analysis; DNA analysis; ss;

KW RNA analysis; RAPD; PCR; primer; random amplified polymorphic DNA.

XX

OS Unidentified.

XX

PN WO200281743-A2.

XX

PD 17-OCT-2002.

XX

XX

PF 28-MAR-2002; 2002WO-GB001489.

XX

PR 02-APR-2001; 2001GB-00008182.

XX

XX (HAMI/) HAMILL B.

PA

PI Hamill B;

XX

XX WPI; 2003-075484/07.

XX

PT Amplification of nucleotide sequences from polynucleotides by chain

PT extension of oligonucleotide primers, comprises 2 oligonucleotides in

PT solution, 2 attached to supports and both share complementary sequences.

XX

PS Disclosure; Fig 17; 60pp; English.

XX

XX The invention comprises a method for the PCR amplification of nucleic

CC acids. The method involves a set of primers, where two of the primers are

CC in solution and at least two other primers are attached to a solid

CC support. The method of the invention can be used for the analysis of a

CC nucleic acid or a mixture of nucleic acids, including: single-stranded

CC DNA molecules, double-stranded DNA molecules and mRNA molecules. The

CC present DNA sequence represents a random amplified polymorphic DNA (RAPD)

CC PCR primer of the invention

XX

SQ Sequence 10 BP; 3 A; 3 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCGGCAT 13

Db 8 GCGGCAT 2

|||||

RESULT 656

ACA62091

ID ACA62091 standard; DNA; 10 BP.

XX

AC ACA62091;

XX

DT 19-AUG-2003 (first entry)

XX

DE Gustductin alpha subunit cloning associated adaptor #2.

XX Taste; taste modification; gustducin alpha subunit;
 KW ligand binding activity; antilgand binding activity;
 KW G protein alpha subunit; conserved region; adaptor; ds.
 XX Synthetic.
 OS
 PN US2003013119-A1.
 XX
 PD 16-JAN-2003.
 XX
 XX 21-FEB-2001; 2001US-00789996.
 XX
 PR 09-APR-1992; 92US-00868353.
 PR 08-APR-1993; 93US-00045801.
 PR 20-MAR-1995; 95US-00407804.
 PR 28-JUL-1998; 98US-00124807.
 PR 20-OCT-1999; 99US-00421796.
 XX
 PA (LING-) LINGUAGEN CORP.
 XX
 PI Margolskee RF;
 XX
 DR WPI; 2003-466043/44.
 XX
 PT Novel gustducin alpha-subunit polypeptide possessing ligand/antilgand
 PT binding activity or immunological property specific to gustducin, for
 PT identifying peptide ligand/antilgand of gustducin and taste modifying
 PT agent.
 XX
 PS Example 1; Page 4; 27pp; English.
 XX
 CC The invention describes a purified and isolated gustducin alpha subunit
 CC polypeptide (I), fragment or variant possessing at least one
 CC ligand/antilgand binding activity or immunological property specific to
 CC gustducin. (I) is useful for identifying a peptide ligand/antilgand of
 CC gustducin, by contacting (I) with peptides and isolating peptides which
 CC bind to (I), and for identifying taste modifying agent. An antibody is
 CC useful for modifying taste which involves delivering Ab to taste receptor
 CC cell. The antibody is useful for purifying (I) and for blocking or
 CC inhibiting ligand/antilgand binding activities of gustducin. This
 CC sequence represents an adaptor used in the cloning of DNA encoding
 CC gustducin alpha subunit
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCGGC 11
 Db 1 GGGCGGC 7
 XX
 RESULT 657
 ACA62967
 ID ACA62967 standard; DNA; 10 BP.
 XX
 AC ACA62967;
 XX
 XX 26-AUG-2003 (first entry)
 DT
 XX DNA sequence for addition to 5' end of primer.
 DE
 XX Corneal epithelium; trefoil protein; intestinal trefoil factor; ITF;
 KW spasmodic peptide; SP; PS2; corneal ulcer; eye surgery;
 KW traumatic physical injury; chemical exposure; peptic ulcer disease;
 KW ultraviolet light exposure; inflammatory bowel disease; eye disorder;
 KW gastrointestinal motility; corneal epithelial wound healing; antiulcer;
 KW antinflammatory; ophthalmological; ds.
 XX
 OS Synthetic.

XX US6525018-B1.
 PN
 XX 25-FEB-2003.
 PD
 XX
 PF 17-MAY-1999; 99US-00313434.
 XX
 PR 17-MAY-1999; 99US-00313434.
 XX
 XX (GEHO) GEN HOSPITAL CORP.
 PA
 XX Podolsky DK;
 PI
 XX WPI; 2003-491768/46.
 DR
 XX Treatment of disruption of corneal epithelium in patient by administering
 PT to the eye of the patient trefoil protein including intestinal trefoil
 PT factor, spasmodic peptide, PS2, or their biological fragments.
 XX
 PS Example 3; Col 13; 31pp; English.
 XX
 CC The present invention relates to a method for the treatment of a
 CC disruption of the corneal epithelium in a patient. The method involves
 CC administering to the patient's eye a trefoil protein including intestinal
 CC trefoil factor (ITF), spasmodic peptide (SP), PS2, or their biological
 CC fragments. The method is useful for the treatment of a disruption of the
 CC corneal epithelium in a patient. It is useful for treating corneal ulcer,
 CC or a disorder caused by traumatic physical injury, eye surgery, chemical
 CC exposure, or ultraviolet light exposure. It can also be used for treating
 CC peptic ulcer diseases, inflammatory bowel diseases, and eye disorders.
 CC The use of intestinal trefoil factor alters gastrointestinal motility in
 CC a mammal or enhances corneal epithelial wound healing. The present DNA
 CC sequence can be added to the 5' end of a primer to engineer a restriction
 CC site
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GGGCGGC 11
 Db 1 GGGCGGC 7
 XX
 RESULT 658
 AAD58326
 ID AAD58326 standard; DNA; 10 BP.
 XX
 AC AAD58326;
 XX
 XX 20-NOV-2003 (first entry)
 DT
 XX GC5 primer used in arbitrarily-primed PCR (AP-PCR) analysis.
 DE
 XX Cell proliferative disorder; central nervous system disorder; infection;
 KW gastrointestinal tract disease; respiratory system disease; inflammation;
 KW sexual malfunction; ulcerative colitis; psychotic disorder; hypertension;
 KW cardiovascular disorder; immune disorder; Hodgkin's disease; drug abuse;
 KW behavioural problem; metabolic disorder; Huntington's disease; dementia;
 KW skin disorder; cancer; lesion; autism; therapy; arbitrarily-primed PCR;
 KW AP-PCR; primer; ss.
 XX
 XX Unidentified.
 OS
 XX WO2003064701-A2.
 PN
 XX 07-AUG-2003.
 PD
 XX 30-JAN-2003; 2003WO-US003000.
 PF
 XX 30-JAN-2002; 2002US-0352944P.
 PR

```

XX (EPiG-) EPIGENOMICS AG.
XX PA
XX PI Sledziewski A, Schweikhardt RG;
XX DR WPI; 2003-618367/58.
XX PT Identifying a reliable diagnostic, prognostic or staging marker for
XX PT phenotypic conditions characterized by altered DNA methylation, e.g.,
XX PT cancer, comprises obtaining a set of at least two biological samples in
XX PT each case having genomic DNA.
XX PS
XX PS Example 1; Page 43; 87pp; English.
XX CC The invention relates to a method for identifying a reliable diagnostic,
XX CC prognostic or staging marker for phenotypic conditions characterised by
XX CC altered DNA methylation. The method involves obtaining a set of at least
XX CC two genomic DNA samples, identifying primary differentially methylated
XX CC CpG dinucleotide sequence positions, selecting a primary differentially
XX CC methylated CpG dinucleotide sequence position and confirming the class-
XX CC distinguishable methylation status of the selected sequence position. The
XX CC method is useful for identifying a reliable diagnostic, prognostic or
XX CC staging marker for phenotypic conditions characterised by altered DNA
XX CC methylation e.g cell proliferative disorders, metabolic disorders,
XX CC central nervous system disorders, immune disorders, cardiovascular
XX CC disorders e.g. hypertension, disease of the respiratory system, sexual
XX CC malfunction, dementia, disease of the gastrointestinal tract, skin
XX CC disorders, lesions, inflammation, infection, drug abuse, behavioural
XX CC problems, psychotic disorders, Hodgkin's disease, cancer, autism,
XX CC ulcerative colitis or Huntington's disease. The method is also useful for
XX CC treating the above mentioned disorders. The present sequence is a primer
XX CC used in arbitrarily-primed PCR (AP-PCR) analysis. This sequence is used
XX CC in the exemplification of the invention
XX SQ
XX Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 4 GGGCGGC 10

RESULT 659
ADA63669
ID ADA63669 standard; DNA; 10 BP.
XX AC ADA63669;
XX DT 20-NOV-2003 (first entry)
XX DE Zinc finger target sequence DNA #433.
XX ds; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.
XX Synthetic.
XX OS
XX PN US2003068675-A1.
XX PD 10-APR-2003.
XX PF 20-NOV-2003 (first entry)
XX DE Zinc finger target sequence DNA #433.
XX ds; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.
XX Synthetic.
XX OS
XX PN US2003068675-A1.
XX PD 10-APR-2003.
XX PF 20-NOV-2003; 2001US-00990186.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX DR WPI; 2003-567233/53.
XX PT Designing zinc finger protein that has three zinc fingers from N-terminus
XX PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
XX PT site, by selecting zinc fingers that bind their respective subsites.
XX PS
XX PS Disclosure; Page 20; 34pp; English.
XX CC The invention relates to a method of designing a zinc finger protein. The
XX CC method is useful for designing a zinc finger protein. The method provides
XX CC multi-finger zinc finger proteins with improved affinity and specificity
XX CC for their target sequences, as well as enhanced biological activity. The
XX CC present sequence represents a zinc finger protein DNA target sequence.
XX SQ
XX Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGCGCA 12
Db 3 GGGCGCA 9

RESULT 660
ADA63670
ID ADA63670 standard; DNA; 10 BP.
XX AC ADA63670;
XX DT 20-NOV-2003 (first entry)
XX DE Zinc finger target sequence DNA #434.
XX ds; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.
XX Synthetic.
XX OS
XX PN US2003068675-A1.
XX PD 10-APR-2003.
XX PF 20-NOV-2001; 2001US-00990186.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX DR WPI; 2003-567233/53.
XX PT Designing zinc finger protein that has three zinc fingers from N-terminus
XX PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
XX PT site, by selecting zinc fingers that bind their respective subsites.
XX PS
XX PS Disclosure; Page 20; 34pp; English.
XX CC The invention relates to a method of designing a zinc finger protein. The
XX CC method is useful for designing a zinc finger protein. The method provides

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XX (LIUQ/) LIU Q.
XX PI Liu Q;
XX DR WPI; 2003-567233/53.
XX PT Designing zinc finger protein that has three zinc fingers from N-terminus
XX PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
XX PT site, by selecting zinc fingers that bind their respective subsites.
XX PS
XX PS Disclosure; Page 20; 34pp; English.
XX CC The invention relates to a method of designing a zinc finger protein. The
XX CC method is useful for designing a zinc finger protein. The method provides
XX CC multi-finger zinc finger proteins with improved affinity and specificity
XX CC for their target sequences, as well as enhanced biological activity. The
XX CC present sequence represents a zinc finger protein DNA target sequence.
XX SQ
XX Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGCGCA 12
Db 3 GGGCGCA 9

RESULT 660
ADA63670
ID ADA63670 standard; DNA; 10 BP.
XX AC ADA63670;
XX DT 20-NOV-2003 (first entry)
XX DE Zinc finger target sequence DNA #434.
XX ds; target sequence; zinc finger protein;
XX multi-finger zinc finger protein; improved affinity;
XX improved specificity; enhanced biological activity.
XX Synthetic.
XX OS
XX PN US2003068675-A1.
XX PD 10-APR-2003.
XX PF 20-NOV-2001; 2001US-00990186.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX PA (LIUQ/) LIU Q.
XX PI Liu Q;
XX DR WPI; 2003-567233/53.
XX PT Designing zinc finger protein that has three zinc fingers from N-terminus
XX PT and C-terminus that bind to subsites in 3' to 5' direction, in a target
XX PT site, by selecting zinc fingers that bind their respective subsites.
XX PS
XX PS Disclosure; Page 20; 34pp; English.
XX CC The invention relates to a method of designing a zinc finger protein. The
XX CC method is useful for designing a zinc finger protein. The method provides

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CC multi-finger zinc finger proteins with improved affinity and specificity
 CC for their target sequences, as well as enhanced biological activity. The
 CC present sequence represents a zinc finger protein DNA target sequence.
 XX
 SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GCGCGCA 12
 |||||
 Db 3 GCGCGCA 9
 RESULT 661
 ADC17777
 ID ADC17777 standard; DNA; 10 BP.
 XX
 AC ADC17777;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 XX Monobactam related tethered diene SEQ ID NO:27.
 DE
 XX
 XX ss; monobactam; antibacterial; PBP2a; inhibitor;
 KW methicillin resistant Staphylococcus aureus; MRSA; lactam antibiotic.
 XX
 OS Synthetic.
 XX
 PN WO2003051314-A2.
 XX
 PD 26-JUN-2003.
 XX
 PF 18-DEC-2002; 2002WO-US040739.
 XX
 PR 18-DEC-2001; 2001US-0340255P.
 XX
 XX (INVE-) INVENUX INC.
 PA
 PI Eaton B, Tarasow T, Nieuwlandt D, Dewey T;
 XX
 XX WPI; 2003-618003/58.
 DR
 XX New monobactam compounds used as antibacterial agents against e.g.
 PT methicillin resistant Staphylococcus aureus.
 PT
 PS Example 6; SEQ ID NO 27; 64pp; English.
 XX
 CC The invention relates to novel monobactam compounds. A compound of the
 CC invention has antibacterial activity, and acts as a PBP2a inhibitor. The
 CC compounds are used as antibacterial agents. The monobactam compounds
 CC restore sensitivity of methicillin resistant Staphylococcus aureus to
 CC lactam antibiotic by targeting the molecular mechanism of resistance. The
 CC present sequence is used in the exemplification of the invention.
 XX
 SQ Sequence 10 BP; 0 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CGCGCGG 7
 |||||
 Db 4 CGCGCGG 10
 RESULT 662
 ADF17248
 ID ADF17248 standard; DNA; 10 BP.
 XX
 AC ADF17248;
 XX

DT 12-FEB-2004 (first entry)
 XX Human intestinal cDNA library associated DNA.
 DE
 XX
 KW antinflammatory; ophthalmological; virucide; fungicide; antibacterial;
 KW eye disorder; intestinal trefoil factor; ITF; spasmolytic peptide; SP;
 KW ps2; superficial punctate keratitis; keratitis sicca; trachoma;
 KW herpes simplex keratoconjunctivitis; ophthalmic herpes zoster;
 KW phlyctenular keratoconjunctivitis; keratoconus; cicatricial pemphigoid;
 KW infection; adenovirus; herpes simplex virus; inflammation;
 KW conjunctival epithelium; scleral epithelium; digestive tract; human;
 KW intestinal cDNA library; ss.
 XX
 OS Synthetic.
 XX
 PN US2003186886-A1.
 XX
 PD 02-OCT-2003.
 XX
 PF 30-MAY-2003; 2003US-00449456.
 XX
 PR 12-APR-1996; 96US-00631469.
 PR 11-APR-1997; 97WO-US006004.
 PR 17-MAY-1999; 99US-00313434.
 PR 06-DEC-2002; 2002US-00313642.
 PR 19-FEB-2003; 2003US-00362310.
 XX
 PA (PODO/) PODOLSKY D K.
 XX
 XX Podolsky DK;
 PI
 XX WPI; 2003-899226/82.
 DR
 XX Treatment of eye disorder comprises administration of trefoil protein
 PT from intestinal trefoil factor, spasmolytic peptide, ps2 or their
 PT biologically active fragments.
 PT
 XX Example 3; Page 7; 36pp; English.
 PS
 XX The invention describes a method of treating an eye disorder comprising
 CC administering to the eye a trefoil protein from intestinal trefoil factor
 CC (ITF), spasmolytic peptide (SP), ps2 or their biologically active
 CC fragments. The method is used for treating eye disorders such as
 CC superficial punctate keratitis, keratitis sicca, trachoma, herpes simplex
 CC keratoconjunctivitis, ophthalmic herpes zoster, phlyctenular
 CC keratoconjunctivitis, keratoconus or cicatricial pemphigoid. The eye
 CC disorder is caused by an infection of bacteria, virus or fungi. The virus
 CC is adenovirus or herpes simplex virus. The eye disorder is inflammation
 CC or conjunctival epithelium or inflammation of the scleral epithelium. The
 CC method provides a protective effect on the digestive tract, and the ITF
 CC promotes the maintenance of mucosal integrity and can also be used to
 CC inhibit adhesion or colonization of the mucosa by Helicobacter pylori.
 CC This sequence represents an oligonucleotide associated with the creation
 CC of a human intestinal cDNA library for isolation of cDNA encoding human
 CC intestinal trefoil factor (ITF). Note: This sequence differs from SEQ ID
 CC NO 5 shown in the sequence listing.
 XX
 SQ Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 GCGCGGC 11
 |||||
 Db 1 GCGCGGC 7
 RESULT 663
 ABZ95037
 ID ABZ95037 standard; DNA; 10 BP.
 XX
 AC ABZ95037;

```

XX 17-OCT-2003 (first entry)
XX Human adenosine A1 receptor antisense fragment no.900.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 10279; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GCGCGGC 8
XX |||||
XX Db 2 GCGCGGC 8
XX
XX RESULT 664
XX ABZ95027
XX ID ABZ95027 standard; DNA; 10 BP.
XX
XX AC ABZ95027;

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XX 17-OCT-2003 (first entry)
XX Human adenosine A1 receptor antisense fragment no.890.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 10269; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 GCGCGGC 8
XX |||||
XX Db 3 GCGCGGC 9
XX
XX RESULT 665
XX ABZ95046
XX ID ABZ95046 standard; DNA; 10 BP.
XX
XX AC ABZ95046;

```

```

XX 17-OCT-2003 (first entry)
XX Human adenosine A1 receptor antisense fragment no.909.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 10288; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGGC 8
DB 1 GCGGGGC 7
RESULT 666
ABZ95816/c
ID ABZ95816 standard; DNA; 10 BP.
XX
XX ABZ95816;
AC

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XX 17-OCT-2003 (first entry)
XX Human adenosine A2b receptor antisense fragment no.1674.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPIG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 11058; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 BP; 0 A; 6 C; 4 G; 0 T; 0 U; 0 Other;
SQ
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GCGGGGC 9
DB 9 GCGGGGC 3
RESULT 667
ABZ95016
ID ABZ95016 standard; DNA; 10 BP.
XX
XX ABZ95016;
AC

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XX 17-OCT-2003 (first entry)
XX Human adenosine A1 receptor antisense fragment no.879.
XX
XX Human; antisense; lung dysfunction; nasal airway dysfunction;
XX antiinflammatory steroid; ubiquinone; antiinflammatory; antiasthmatic;
XX antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
XX antisense gene therapy; respiratory; lung; adenosine sensitivity;
XX adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
XX lung inflammation; respiratory disease; ds.
XX
XX Homo sapiens.
XX
XX WO200285308-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US013135.
XX
XX 24-APR-2001; 2001US-0286137P.
XX
XX (EPITG-) EPIGENESIS PHARM INC.
XX
XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
XX Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-229219/22.
XX
XX Pharmaceutical composition for treating ailments associated with impaired
XX respiration, has oligo(s) antisense to specific gene(s) or its
XX corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
XX ubiquinone.
XX
XX Disclosure; SEQ ID NO 10258; 872pp; English.
XX
XX The invention relates to a novel pharmaceutical composition, which has a
XX first active agent comprising an oligonucleotide antisense to the
XX initiation codon, coding region, 5' or 3' end genomic flanking regions,
XX 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
XX junctions of genes encoding a polypeptide associated with lung and/or
XX nasal airway dysfunction and a second active agent comprising an
XX antiinflammatory steroid and ubiquinone. A composition of the invention
XX has antiinflammatory, antiasthmatic, antiasthmatic, hypotensive,
XX immunosuppressive, and cytostatic activity. The composition may have a
XX use in antisense gene therapy. The composition is useful for treating or
XX preventing a respiratory, lung or malignant disease or condition, also
XX for enhancing the prophylactic or therapeutic respiratory effect of an
XX antiinflammatory steroid in a subject, for reducing or depleting levels
XX of, or reducing sensitivity to adenosine, reducing levels of adenosine
XX receptor, producing bronchodilation, increasing levels of ubiquinone or
XX lung surfactant in a subject's tissue, or treating bronchoconstriction,
XX lung inflammation, lung allergies, or a respiratory disease or condition.
XX Note: The sequence data for this patent is not represented in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences
XX
XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
    Query Match      43.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 3.4e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGGC 8
Db 4 GCGCGGC 10
    |||||
    |||||

RESULT 668
ABX11772
ID ABX11772 standard; DNA; 10 BP.
XX
XX ABX11772;
AC

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```

XX 10-MAY-2003 (first entry)
XX Human K-RAS oncogene DNA nucleotides 138-147.
XX
XX Human; cancer; colon cancer; haematologic cancer; lung cancer;
XX prostate cancer; skin cancer; thyroid cancer; ovarian cancer;
XX K-RAS oncogene; K-RAS expression; cancer cell proliferation;
XX mutation-activated K-RAS expression; cytostatic; ds.
XX
XX Homo sapiens.
XX
XX US2002165196-A1.
XX
XX 07-NOV-2002.
XX
XX 07-MAY-2002; 2002US-00141263.
XX
XX 07-MAY-2001; 2001US-0289166P.
XX
XX (WICK/) WICKSTROM E.
XX
XX Wickstrom E;
XX
XX WPI; 2003-288145/28.
XX
XX Preventing or treating cancer, e.g. colon cancer, lung cancer or ovarian
XX cancer, comprises administering to a mammal an oligonucleotide targeted
XX to a nucleic acid encoding human K-RAS oncogene, and modulating K-RAS
XX expression.
XX
XX Disclosure; Page 10; 14pp; English.
XX
XX The present invention relates to a method for preventing or treating
XX cancers, such as colon, haematologic, lung, prostate, skin, thyroid, or
XX preferably ovarian cancer. The method comprises administering an
XX antisense oligonucleotide targeted to a nucleic acid encoding human K-RAS
XX oncogene, and modulating K-RAS expression. The oligonucleotides and
XX method of the invention inhibit cancer cell proliferation, and are useful
XX for preventing or treating cancers such as those mentioned above. The
XX oligonucleotides are also useful for research purposes, or for modulating
XX mutation-activated K-RAS expression in ovarian, colon, lung, thyroid,
XX prostate, skin, or haematologic cancer cells. The present sequence
XX represents human K-RAS oncogene DNA nucleotides 138-147 to which
XX antisense oligonucleotides can be targeted
XX
XX Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;
    Query Match      43.8%; Score 7; DB 1; Length 10;
    Best Local Similarity 100.0%; Pred. No. 3.4e+02;
    Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGG 7
Db 2 CGCGCGG 8
    |||||
    |||||

RESULT 669
ABX11773/C
ID ABX11773 standard; DNA; 10 BP.
XX
XX ABX11773;
AC
XX
XX 10-MAY-2003 (first entry)
XX
XX Human K-RAS oncogene antisense oligonucleotide KRAS8.
XX
XX Human; cancer; colon cancer; haematologic cancer; lung cancer;
XX prostate cancer; skin cancer; thyroid cancer; ovarian cancer;
XX K-RAS oncogene; K-RAS expression; cancer cell proliferation;
XX mutation-activated K-RAS expression; cytostatic; antisense; ss.
XX
XX Homo sapiens.

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XX PN US2002165196-A1.
XX XX
XX PD 07-NOV-2002.
XX XX
XX PF 07-MAY-2002; 2002US-00141263.
XX XX
XX PR 07-MAY-2001; 2001US-0289166P.
XX XX
XX PA (WICK/) WICKSTROM E.
XX XX
XX PI Wickstrom E;
XX XX
XX DR WPI; 2003-288145/28.
XX XX
XX PT Preventing or treating cancer, e.g. colon cancer, lung cancer or ovarian
XX PT cancer, comprises administering to a mammal an oligonucleotide targeted
XX PT to a nucleic acid encoding human K-RAS oncogene, and modulating K-RAS
XX PT expression.
XX PS Claim 19; Page 4; 14pp; English.
XX XX
XX CC The present invention relates to a method for preventing or treating
XX CC cancers, such as colon, haematologic, lung, prostate, skin, thyroid, or
XX CC preferably ovarian cancer. The method comprises administering an
XX CC antisense oligonucleotide targeted to a nucleic acid encoding human K-RAS
XX CC oncogene, and modulating K-RAS expression. The oligonucleotides and
XX CC method of the invention inhibit cancer cell proliferation, and are useful
XX CC for preventing or treating cancers such as those mentioned above. The
XX CC oligonucleotides are also useful for research purposes, or for modulating
XX CC mutation-activated K-RAS expression in ovarian, colon, lung, thyroid,
XX CC prostate, skin, or haematologic cancer cells. The present sequence
XX CC represents an antisense oligonucleotide of the invention
XX SQ Sequence 10 BP; 0 A; 7 C; 3 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGG 7
Db 9 CGCGCGG 3

RESULT 670
ADM22167
ID ADM22167 standard; DNA; 10 BP.
XX AC
XX AD ADM22167;
XX DT 20-MAY-2004 (first entry)
XX DE Synthetic zinc finger protein target DNA #433.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX XX
XX PN US2003104526-A1.
XX XX
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX XX
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX OS Unidentified.
XX XX
XX PN US2003104526-A1.
XX XX
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX XX
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX XX
XX PA (LIU/) LIU Q.
XX PI
XX DR WPI; 2003-843091/78.
XX XX
XX PT New zinc finger protein used for recognizing triplet target subsites
XX PT having nucleotide G in 5'-most position of subsite, that has been
XX PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1641; 48pp; English.
XX XX
XX CC The invention describes a new zinc finger protein that binds to a target

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XX PI Liu Q;
XX DR WPI; 2003-843091/78.
XX XX
XX PT New zinc finger protein used for recognizing triplet target subsites
XX PT having nucleotide G in 5'-most position of subsite, that has been
XX PT optimized with respect to location of subsite within target site.
XX XX
XX PS Example 6; SEQ ID NO 1640; 48pp; English.
XX XX
XX CC The invention describes a new zinc finger protein that binds to a target
XX CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
XX CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
XX CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
XX CC (S3) target subsites. The zinc finger proteins can be used for
XX CC recognising triplet target subsites having the nucleotide G in the 5'-
XX CC most position of the subsite, that has been optimised with respect to the
XX CC location of the subsite within the target site. This sequence represents
XX CC the target polynucleotide of a synthetic zinc finger protein of the
XX CC invention.
XX SQ Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
Db 3 GCGCGCA 9

RESULT 671
ADM22168
ID ADM22168 standard; DNA; 10 BP.
XX AC
XX AD ADM22168;
XX DT 20-MAY-2004 (first entry)
XX DE Synthetic zinc finger protein target DNA #434.
XX KW zinc finger protein; triplet target subsite; zinc finger motif; sp-1; ds.
XX OS Unidentified.
XX XX
XX PN US2003104526-A1.
XX XX
XX PD 05-JUN-2003.
XX PF 20-NOV-2001; 2001US-00989994.
XX XX
XX PR 24-MAR-1999; 99US-0126238P.
XX PR 24-MAR-1999; 99US-0126239P.
XX PR 30-JUL-1999; 99US-0146595P.
XX PR 30-JUL-1999; 99US-0146615P.
XX PR 23-MAR-2000; 2000US-00535008.
XX PR 20-NOV-2000; 2000US-00716637.
XX XX
XX PA (LIU/) LIU Q.
XX PI
XX DR WPI; 2003-843091/78.
XX XX
XX PT New zinc finger protein used for recognizing triplet target subsites
XX PT having nucleotide G in 5'-most position of subsite, that has been
XX PT optimized with respect to location of subsite within target site.
XX PS Example 6; SEQ ID NO 1641; 48pp; English.
XX XX
XX CC The invention describes a new zinc finger protein that binds to a target

```

CC site comprising a first (F1), a second (F2) or a third (F3) zinc finger,
 CC ordered F1, F2 and F3 from N-terminus to C-terminus. The target site
 CC comprises, in the 3' to 5' direction, first (S1), second (S2) and third
 CC (S3) target subunits. The zinc finger proteins can be used for
 CC recognising triplet target subunits having the nucleotide G in the 5'-
 CC most position of the subunit, that has been optimised with respect to the
 CC location of the subunit within the target site. This sequence represents
 CC the target polynucleotide of a synthetic zinc finger protein of the
 CC invention.

XX Sequence 10 BP; 1 A; 3 C; 6 G; 0 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGCGGCA 12
 Db 3 GGCGGCA 9
 |||||

RESULT 672
 ADM29239
 ID ADM29239 standard; DNA; 10 BP.
 XX AC
 AC ADM29239;
 XX DT
 DT 20-MAY-2004 (first entry)
 XX DE
 DE NotI site for cDNA cloning.

XX NotI; ss; intestinal trefoil factor; pancreatic spasmolytic peptide; PSP;
 KW ps2; antiinflammatory; ophthalmological; antibacterial; antiemetic;
 KW cytotatic; immunosuppressive; tranquiliser; vulnerary; antiapoptotic;
 KW eye epithelium; microbial infection; viral infection;
 KW bacterial infection; fungal infection; adenoviral infection;
 KW herpes simplex virus infection; eye disease; corneal ulcer;
 KW ocular inflammatory disease; corneal epithelial wound healing;
 KW digestive tract disorder; gastritis; ulcer; gastric cancer;
 KW MALT lymphoma; Menetrier's disease; inflammatory bowel disease.

XX Synthetic.
 OS
 XX US2003134797-A1.
 PN
 XX 17-JUL-2003.
 PD
 XX 06-DEC-2002; 2002US-00313642.
 PF
 XX 17-MAY-1999; 99US-00313434.
 PR
 XX (PODO/) PODOLSKY D K.
 PA
 XX Podolsky DK;
 PI
 XX WPI; 2003-897264/82.
 DR
 XX Treating disruption of epithelium of patient's eye comprises
 PT administering trefoil protein, e.g. intestinal trefoil factor to
 PT patient's eye.
 PS Example 3; SEQ ID NO 5; 33pp; English.

XX The invention relates to treating the disruption of the epithelium of the
 CC eye in a patient comprising administering a trefoil protein to the eye of
 CC the patient. The trefoil protein is intestinal trefoil factor (ITF),
 CC pancreatic spasmolytic peptide (PSP), ps2 or their biologically active
 CC fragments. The disruption is caused by microbial infection (viral,
 CC bacterial, or fungal infection). The viral infection is adenoviral
 CC infection or herpes simplex virus infection. The trefoil proteins of the
 CC invention are resistant to destruction in the digestive tract and
 CC effectively treat eye diseases (e.g. corneal ulcer, ocular inflammatory
 CC disease) and have the ability to enhance corneal epithelial wound

CC healing. The proteins are also useful in treating digestive tract
 CC disorders e.g. gastritis, ulcers, gastric cancer, MALT lymphoma,
 CC Menetrier's disease and inflammatory bowel disease. The present sequence
 CC is a NotI site which may be engineered onto isolated cDNA to facilitate
 CC cloning.

XX Sequence 10 BP; 0 A; 4 C; 6 G; 0 T; 0 U; 0 Other;
 SQ Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGC 11
 Db 1 GGCGGC 7
 |||||

RESULT 673
 ABD18875
 ID ABD18875 standard; DNA; 10 BP.
 XX AC
 AC ABD18875;
 XX DT
 DT 29-JUL-2004 (first entry)
 XX DE
 DE Human adenosine A1 receptor oligonucleotide fragment 890.

XX Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 KW analgesic; hypotensive; immunosuppressive; cytotatic; cystic fibrosis;
 KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 KW pulmonary transplantation rejection; ds.

XX Homo sapiens.
 OS
 XX WO200285309-A2.
 PN
 XX 31-OCT-2002.
 PD
 XX 23-APR-2002; 2002WO-US013143.
 PF
 XX 24-APR-2001; 2001US-0286036P.
 PR
 XX (EPIG-) EPIGENESIS PHARM INC.
 PA
 XX Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 PI Miller S, Tang L, Shahabuddin S;
 XX WPI; 2003-093058/08.
 DR
 XX Pharmaceutical composition for treating asthma, has antisense
 PT oligonucleotide containing less percentage of adenosine, targeted to
 PT nucleic acids associated with lung airway or lung dysfunction, and
 PT bronchodilating agent.

XX Claim 15; SEQ ID NO 10269; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,
 CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies, asthma, and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC the oligonucleotides in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 CC Sequence 10 BP; 2 A; 2 C; 5 G; 1 T; 0 U; 0 Other;
 CC
 CC Query Match 43.8%; Score 7; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 GCGGGC 8
 CC DB 3 GCGGGC 9
 CC
 CC RESULT 674
 CC ABD18885
 CC ID ABD18885 standard; DNA; 10 BP.
 CC AC ABD18885;
 CC DT 29-JUL-2004 (first entry)
 CC XX Human adenosine A1 receptor oligonucleotide fragment 900.
 CC
 CC Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 CC respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 CC surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 CC analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 CC beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 CC respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 CC emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 CC pulmonary transplantation rejection; ds.
 CC
 CC OS Homo sapiens.
 CC XX WO200285309-A2.
 CC XX 31-OCT-2002.
 CC XX 23-APR-2002; 2002WO-US013143.
 CC XX 24-APR-2001; 2001US-0286036P.
 CC XX (EPIG-) EPIGENESIS PHARM INC.
 CC
 CC Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
 CC Miller S, Tang L, Shahabuddin S;
 CC WPI; 2003-093058/08.
 CC
 CC Pharmaceutical composition for treating asthma, has antisense
 CC oligonucleotide containing less percentage of adenosine, targeted to
 CC nucleic acids associated with lung airway or lung dysfunction, and
 CC bronchodilating agent.
 CC
 CC Claim 15; SEQ ID NO 10279; 763pp; English.
 CC
 CC This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating
 CC bronchoconstriction, respiratory tract inflammation, allergies and
 CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
 CC surfactant depletion or hyposecretion, when administered to a mammal. The
 CC oligonucleotides are derived from a gene encoding or regulating
 CC expression of a target polypeptide associated with lung airway or lung
 CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
 CC The invention also describes a kit, that comprises: (a) a delivery
 CC device, in separate containers, (b) the oligonucleotides, (c)
 CC instructions for adding a carrier and for use of the kit. The composition
 CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
 CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
 CC beta-adrenergic agonist. The composition is useful for preventing or
 CC treating a respiratory, lung or malignant disease. The administered
 CC composition comprises oligo and is administered to reduce the production
 CC or availability, or to increase the degradation of the target mRNA or to
 CC reduce the amount of target polypeptide present in the lungs. The
 CC pulmonary obstruction, and/or bronchoconstriction and/or lung
 CC inflammation, allergies and/or surfactant hypoproduction are associated
 CC with a disease or condition such as pulmonary vasoconstriction,
 CC inflammation, allergies, asthma, impeded respiration, respiratory
 CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
 CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
 CC transplantation rejection, pulmonary infections, bronchitis or cancer.
 CC The reduced adenosine content of the anti-sense oligos corresponding to
 CC the oligonucleotides in the target RNA serves to prevent the breakdown of
 CC the oligonucleotides into products that free adenosine into the system
 CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
 CC prevent any unwanted effects due to it
 CC
 CC Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
 CC
 CC Query Match 43.8%; Score 7; DB 1; Length 10;
 CC Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 CC Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 CC QY 2 GCGGGC 8
 CC DB 2 GCGGGC 8
 CC
 CC RESULT 675
 CC ABD18864
 CC ID ABD18864 standard; DNA; 10 BP.
 CC AC ABD18864;
 CC XX 29-JUL-2004 (first entry)
 CC XX Human adenosine A1 receptor oligonucleotide fragment 879.
 CC
 CC Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
 CC respiratory tract inflammation; adenosine sensitivity; lung; cancer;
 CC surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
 CC analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
 CC beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
 CC respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
 CC emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
 CC pulmonary transplantation rejection; ds.
 CC
 CC OS Homo sapiens.
 CC XX WO200285309-A2.
 CC XX 31-OCT-2002.
 CC XX 23-APR-2002; 2002WO-US013143.
 CC XX 24-APR-2001; 2001US-0286036P.
 CC XX (EPIG-) EPIGENESIS PHARM INC.
 CC
 CC Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;

```

PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX Claim 15; SEQ ID NO 10258; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGGC 8
Db |||||
4 GCGGGGC 10
RESULT 676
ABD18967/c
ID ABD18967 standard; DNA; 10 BP.
XX AC ABD18967;
XX DT 29-JUL-2004 (first entry)
XX Human adenosine A2b receptor oligonucleotide fragment 1674.
DE Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
XX respiratory tract inflammation; adenosine sensitivity; lung; cancer;
XX surfactant depletion; anti-allergic; anti-inflammatory; antiasthmatic;
XX analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
XX beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
XX respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
XX emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
XX pulmonary transplantation rejection; ds.
XX Homo sapiens.
PI Miller S, Tang L, Shahabuddin S;
XX WPI; 2003-093058/08.
XX Pharmaceutical composition for treating asthma, has antisense
XX oligonucleotide containing less percentage of adenosine, targeted to
XX nucleic acids associated with lung airway or lung dysfunction, and
XX bronchodilating agent.
XX Claim 15; SEQ ID NO 10258; 763pp; English.
XX This invention describes a novel composition (a) a first active agent,
XX comprising oligonucleotides, effective for alleviating
XX bronchoconstriction, respiratory tract inflammation, allergies and
XX reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
XX surfactant depletion or hyposecretion, when administered to a mammal. The
XX oligonucleotides are derived from a gene encoding or regulating
XX expression of a target polypeptide associated with lung airway or lung
XX dysfunction or cancer and can be anti-sense to the corresponding mRNA.
XX The invention also describes a kit, that comprises: (a) a delivery
XX device, in separate containers, (b) the oligonucleotides, (c)
XX instructions for adding a carrier and for use of the kit. The composition
XX of the invention has anti-allergic, anti-inflammatory, antiasthmatic,
XX analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
XX beta-adrenergic agonist. The composition is useful for preventing or
XX treating a respiratory, lung or malignant disease. The administered
XX composition comprises oligo and is administered to reduce the production
XX or availability, or to increase the degradation of the target mRNA or to
XX reduce the amount of target polypeptide present in the lungs. The
XX pulmonary obstruction, and/or bronchoconstriction and/or lung
XX inflammation, allergies and/or surfactant hypoproduction are associated
XX with a disease or condition such as pulmonary vasoconstriction,
XX inflammation, allergies, asthma, impeded respiration, respiratory
XX distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
XX hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
XX transplantation rejection, pulmonary infections, bronchitis or cancer.
XX The reduced adenosine content of the anti-sense oligos corresponding to
XX thymidines present in the target RNA serves to prevent the breakdown of
XX the oligonucleotides into products that free adenosine into the system
XX e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
XX prevent any unwanted effects due to it
XX Sequence 10 BP; 1 A; 3 C; 5 G; 1 T; 0 U; 0 Other;
SQ Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGGGGC 8
Db |||||
4 GCGGGGC 10
RESULT 677
ABD18894
ID ABD18894 standard; DNA; 10 BP.
XX AC ABD18894;
XX DT 29-JUL-2004 (first entry)
XX Homo sapiens.

```

DE Human adenosine A1 receptor oligonucleotide fragment 909.

XX Human; antiseizure; bronchoconstriction; allergy; hyposecretion; pain;

KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;

KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;

KW analgesic; hypotensive; immunosuppressive; cytosstatic; cystic fibrosis;

KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;

KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;

KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

KW pulmonary transplantation rejection; ds.

XX Homo sapiens.

OS WO200285309-A2.

XX 31-OCT-2002.

XX 23-APR-2002; 2002WO-US013143.

XX 24-APR-2001; 2001US-0286036P.

XX (EPIC-) EPIGENESIS PHARM INC.

PA Nyce JW, Li Y, Sandraagra A, Katz E, Pabalan J, Aguilar D;

PI Miller S, Tang L, Shahabuddin S;

PI WPI; 2003-093058/08.

DR Pharmaceutical composition for treating asthma, has antiseizure

XX oligonucleotide containing less percentage of adenosine, targeted to

PT nucleic acids associated with lung airway or lung dysfunction, and

PT bronchodilating agent.

XX Claim 15; SEQ ID NO 10288; 763pp; English.

XX This invention describes a novel composition (a) a first active agent,

CC comprising oligonucleotides, effective for alleviating

CC bronchoconstriction, respiratory tract inflammation, allergies and

CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,

CC surfactant depletion or hyposecretion, when administered to a mammal. The

CC oligonucleotides are derived from a gene encoding or regulating

CC expression of a target polypeptide associated with lung airway or lung

CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.

CC The invention also describes a kit, that comprises: (a) a delivery

CC device, in separate containers, (b) the oligonucleotides, (c)

CC instructions for adding a carrier and for use of the kit. The composition

CC of the invention has antiallergic, antiinflammatory, antiasthmatic,

CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a

CC beta-adrenergic agonist. The composition is useful for preventing or

CC treating a respiratory, lung or malignant disease. The administered

CC composition comprises oligo and is administered to reduce the production

CC or availability, or to increase the degradation of the target mRNA or to

CC reduce the amount of target polypeptide present in the lungs. The

CC pulmonary obstruction, and/or bronchoconstriction and/or lung

CC inflammation, allergies and/or surfactant hypoproduction are associated

CC with a disease or condition such as pulmonary vasoconstriction,

CC inflammation, allergies, asthma, impeded respiration, respiratory

CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary

CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary

CC transplantation rejection, pulmonary infections, bronchitis or cancer.

CC The reduced adenosine content of the anti-sense oligos corresponding to

CC thymidines present in the target RNA serves to prevent the breakdown of

CC the oligonucleotides into products that free adenosine into the system

CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to

CC prevent any unwanted effects due to it

XX Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8

DE RESULT 679

ADH57601/c

ID ADH57601 standard; DNA; 10 BP.

XX

AC ADH57601;

Db |||||

1 GCGGGGC 7

RESULT 678

ADH57613/c

ID ADH57613 standard; DNA; 10 BP.

XX

AC ADH57613;

XX 25-MAR-2004 (first entry)

XX Extendable oligo E102 for DNA sequencing and PCR amplification.

DE ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;

XX rolling circle amplification; strand displacement amplification;

KW isothermal DNA amplification; biotechnology; agriculture;

KW medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.

XX Synthetic.

OS WO2003093500-A1.

PN 13-NOV-2003.

XX 24-DEC-2002; 2002WO-AU001763.

XX 01-MAY-2002; 2002AU-00002045.

XX (NUCL-) NUCLEICS PTY LTD.

PA Tillett D, Thomas T;

PI WPI; 2004-053046/05.

DR Increasing the affinity of an extendable oligonucleotide (EO) for a

XX target nucleic acid, for providing primers having improved specificity,

PT comprises hybridization of the EO to a template oligonucleotide (TO) and

PT extension of the EO.

XX Example 9; Page 41; 85pp; English.

XX This invention relates to a novel method for the optimisation of primer

CC libraries. Specifically, it refers to increasing the affinity of short

CC oligonucleotide primers, also known as extendable oligos (EOs), for their

CC template sequences. The present invention describes improved methods for

CC sequencing and the linear and exponential amplification of DNA that can

CC be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle

CC amplification, strand displacement amplification and isothermal DNA

CC amplification. Accordingly, these extendable oligos with improved

CC specificity and affinity are particularly important in fields ranging

CC from biotechnology and agriculture to medical research. This

CC oligonucleotide sequence is an extendable oligonucleotide that includes

CC an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch

CC region, and is useful for both DNA sequencing reactions and PCR

CC amplification in an exemplification of the invention.

XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCGGGGC 10

Db |||||

10 GCGGGGC 4

RESULT 679

ADH57601/c

ID ADH57601 standard; DNA; 10 BP.

XX

AC ADH57601;

```

XX 25-MAR-2004 (first entry)
XX Extendable oligo E090 for DNA sequencing and PCR amplification.
XX
XX ss; primer library; extendable oligo; EO; ligation chain reaction; LCR;
XX rolling circle amplification; strand displacement amplification;
XX isothermal DNA amplification; biotechnology; agriculture;
XX medical research; 2,4 diaminopurine nucleotide analogue; PCR; primer.
XX
XX Synthetic.
XX
XX WO2003093500-A1.
XX
XX 13-NOV-2003.
XX
XX 24-DEC-2002; 2002WO-AU001763.
XX
XX 01-MAY-2002; 2002AU-00002045.
XX
XX (NUCL-) NUCLEICS PTY LTD.
XX
XX Tillett D, Thomas T;
XX
XX WPI; 2004-053046/05.
XX
XX Increasing the affinity of an extendable oligonucleotide (EO) for a
XX target nucleic acid, for providing primers having improved specificity,
XX comprises hybridization of the EO to a template oligonucleotide (TO) and
XX extension of the EO.
XX
XX Example 9; Page 40; 85pp; English.
XX
XX This invention relates to a novel method for the optimisation of primer
XX libraries. Specifically, it refers to increasing the affinity of short
XX oligonucleotide primers, also known as extendable oligos (EOs), for their
XX template sequences. The present invention describes improved methods for
XX sequencing and the linear and exponential amplification of DNA that can
XX be useful for PCR, RT-PCR, ligation chain reaction (LCR), rolling circle
XX amplification, strand displacement amplification and isothermal DNA
XX amplification. Accordingly, these extendable oligos with improved
XX specificity and affinity are particularly important in fields ranging
XX from biotechnology and agriculture to medical research. This
XX oligonucleotide sequence is an extendable oligonucleotide that includes
XX an adenine replacement 2,4 diaminopurine nucleotide analogue in the catch
XX region, and is useful for both DNA sequencing reactions and PCR
XX amplification in an exemplification of the invention.
XX
XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CGGCGGG 7
XX |
XX 10 CGGCGGG 4
XX
XX RESULT 680
XX ADS76874
XX ID ADS76874 standard; DNA; 10 BP.
XX
XX AC ADS76874;
XX
XX 30-DEC-2004 (first entry)
XX
XX Breast cancer detection oligonucleotide #656.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 2; SEQ ID NO 656; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 GGCGGGC 8
XX |
XX 3 GGCGGGC 9
XX
XX RESULT 681
XX ADS77539/c
XX ID ADS77539 standard; DNA; 10 BP.
XX
XX AC ADS77539;
XX
XX 30-DEC-2004 (first entry)
XX
XX Breast cancer detection oligonucleotide #1321.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.

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KW collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.
XX
XX Polyak K, Porter D, Allinen M;
XX
XX WPI; 2004-728732/71.
XX
XX Diagnosing breast cancer comprises determining expression levels of a
XX gene selected from those differentially expressed in normal or cancerous
XX cells of a breast tissue sample including interleukin 1, thrombospondin 1
XX and cystatin C.
XX
XX Example 2; SEQ ID NO 656; 149pp; English.
XX
XX The invention relates to a method of diagnosis (M1) comprising: (a)
XX providing a test sample of breast tissue; (b) determining the level of
XX expression in the test sample of a gene (e.g. interleukin-8, superoxide
XX dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
XX specification, and (c) if the gene is expressed in the test sample at a
XX lower level than in a control normal breast tissue sample, diagnosing the
XX test sample as containing cancer cells. The method is used for diagnosing
XX breast cancer. This sequence corresponds to an oligonucleotide primer
XX used in the method of the invention.
XX
XX Sequence 10 BP; 1 A; 2 C; 6 G; 1 T; 0 U; 0 Other;
XX
XX Query Match 43.8%; Score 7; DB 1; Length 10;
XX Best Local Similarity 100.0%; Pred. No. 3.4e+02;
XX Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 GGCGGGC 8
XX |
XX 3 GGCGGGC 9
XX
XX RESULT 681
XX ADS77539/c
XX ID ADS77539 standard; DNA; 10 BP.
XX
XX AC ADS77539;
XX
XX 30-DEC-2004 (first entry)
XX
XX Breast cancer detection oligonucleotide #1321.
XX
XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
XX antisense oligonucleotide inhibitor; cathepsin K inhibitor;
XX cathepsin L inhibitor; cathepsin F inhibitor;
XX metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
XX collagen antagonist; diagnosis; breast tissue; cancer.
XX
XX Homo sapiens.
XX
XX WO2004085621-A2.
XX
XX 07-OCT-2004.
XX
XX 22-MAR-2004; 2004WO-US008866.
XX
XX 20-MAR-2003; 2003US-0456735P.
XX
XX (DAND ) DANA FARBER CANCER INST INC.

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XX PI Polyak K, Porter D, Allinen M;
 XX WPI; 2004-728732/71.
 XX Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX Example 6; SEQ ID NO 1321; 149pp; English.
 XX
 XX The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
 Db 7 GGGCGGC 1

RESULT 682
 ADS77304/c
 ID ADS77304 standard; DNA; 10 BP.
 XX
 XX AC ADS77304;
 XX
 XX 30-DEC-2004 (first entry)
 XX
 XX Breast cancer detection oligonucleotide #1086.
 XX
 XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 XX Homo sapiens.
 XX
 XX WO2004085621-A2.
 XX
 XX 07-OCT-2004.
 XX
 XX 22-MAR-2004; 2004WO-US008866.
 XX
 XX 20-MAR-2003; 2003US-0456735P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 XX
 XX Polyak K, Porter D, Allinen M;
 XX
 XX WPI; 2004-728732/71.
 XX
 XX Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX Example 2; SEQ ID NO 1086; 149pp; English.
 XX
 XX The invention relates to a method of diagnosis (M1) comprising: (a)

CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
 Db 7 GGGCGGC 1

RESULT 683
 ADS77303/c
 ID ADS77303 standard; DNA; 10 BP.
 XX
 XX AC ADS77303;
 XX
 XX 30-DEC-2004 (first entry)
 XX
 XX Breast cancer detection oligonucleotide #1085.
 XX
 XX ss; primer; cytostatic; RNA interference; RNAi; gene silencing;
 KW antisense oligonucleotide inhibitor; cathepsin K inhibitor;
 KW cathepsin L inhibitor; cathepsin F inhibitor;
 KW metalloprotease 2 inhibitor; thrombospondin-2 antagonist;
 KW collagen antagonist; diagnosis; breast tissue; cancer.
 XX
 XX Homo sapiens.
 XX
 XX WO2004085621-A2.
 XX
 XX 07-OCT-2004.
 XX
 XX 22-MAR-2004; 2004WO-US008866.
 XX
 XX 20-MAR-2003; 2003US-0456735P.
 XX
 XX (DAND) DANA FARBER CANCER INST INC.
 XX
 XX Polyak K, Porter D, Allinen M;
 XX
 XX WPI; 2004-728732/71.
 XX
 XX Diagnosing breast cancer comprises determining expression levels of a
 PT gene selected from those differentially expressed in normal or cancerous
 PT cells of a breast tissue sample including interleukin 1, thrombospondin 1
 PT and cystatin C.
 XX
 XX Example 2; SEQ ID NO 1085; 149pp; English.
 XX
 XX The invention relates to a method of diagnosis (M1) comprising: (a)
 CC providing a test sample of breast tissue; (b) determining the level of
 CC expression in the test sample of a gene (e.g. interleukin-8, superoxide
 CC dismutase 2 and tubulin, alpha 3) selected from Table 1 given in the
 CC specification, and (c) if the gene is expressed in the test sample at a
 CC lower level than in a control normal breast tissue sample, diagnosing the
 CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.
 XX
 XX Sequence 10 BP; 0 A; 6 C; 3 G; 1 T; 0 U; 0 Other;
 SQ

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;

CC test sample as containing cancer cells. The method is used for diagnosing
 CC breast cancer. This sequence corresponds to an oligonucleotide primer
 CC used in the method of the invention.

XX SQ Sequence 10 BP; 1 A; 5 C; 4 G; 0 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGGCGGG 7
 |||||
 Db 8 CGGCGGG 2

RESULT 689

ID ADU18811 standard; DNA; 10 BP.

XX AC ADU18811;

XX DT 13-JAN-2005 (first entry)

XX DE Hypoxia-related tumorigenesis-related SAGE tag #602.

XX screening; hypoxia-related tumorigenesis;

KW hypoxia-induced gene regulation; tumour; SAGE tag; ds.

KW Unidentified.

OS WO2004092198-A2.

XX FN 28-OCT-2004.

XX PD 09-APR-2004; 2004WO-US011087.

XX PF 09-APR-2003; 2003US-0461712P.

XX PR (GENZ) GENZYME CORP.

XX PA Nacht M;

XX PI WPI; 2004-758333/74.

XX DR Identifying agents that alter biological activity of a polypeptide
 XX encoded by a polynucleotide involved in hypoxia-related tumorigenesis
 PT comprises contacting an agent with a target cell and monitoring activity
 PT of expressed product.

XX PS Disclosure; Page 67; 100pp; English.

XX CC The invention comprises a method of screening for candidate agents
 CC capable of altering the biological activity of a protein encoded by a
 CC nucleotide involved in hypoxia-related tumorigenesis. The method of the
 CC invention involves: contacting a test agent with a target cell expressing
 CC the nucleotide, and monitoring the activity of the expressed protein
 CC product; if the test agent modifies the activity of the expressed protein
 CC then this is a candidate agent. The method of the invention is useful for
 CC modifying hypoxia-induced gene regulation and for diagnosing, prognosing
 CC or treating tumours. The present DNA sequence represents a SAGE tag that
 CC was used in the exemplification of the invention.

XX SQ Sequence 10 BP; 0 A; 3 C; 6 G; 1 T; 0 U; 0 Other;
 Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 GGGCGGC 11
 |||||
 Db 4 GGGCGGC 10

RESULT 690

ADW10555

ID ADW10555 standard; DNA; 10 BP.

XX AC ADW10555;

XX DT 24-MAR-2005 (first entry)

XX DE Human genomic DNA fragment arbitrarily-primed PCR primer, GC5.

XX KW colorectal tumor; CpG methylation detection; cytostatic; gene therapy;
 KW proliferative disorder; carcinoma; PCR; primer; ss.

XX OS Homo sapiens.

XX OS Synthetic.

XX PN US2004265833-A1.

XX PD 30-DEC-2004.

XX PF 23-JUN-2003; 2003US-00602494.

XX PR 23-JUN-2003; 2003US-00602494.

XX PA (LOFT/) LOFTON-DAY C.

XX PA (SLED/) SLEDZIEWSKI A.

XX PA (THOM/) THOMAS J.

XX PA (DAYR/) DAY R W.

XX PA (TONN/) TONNES-PRIDY L.

XX PA (CARD/) CARDON K.

XX XX Lofton-Day C, Sledziewski A, Thomas J, Day RW, Tonnes-Priddy L;
 PI Cardon K;

XX WPI; 2005-089566/10.

XX DR Detecting and distinguishing colorectal cell proliferative disorders by
 XX contacting genomic DNA of biological sample with reagent that
 PT distinguishes methylated and non-methylated CpG dinucleotides within
 PT target sequence of genomic DNA.

XX PS Example 1; SEQ ID NO 360; 23pp; English.

XX CC The invention relates to a novel method for detecting and distinguishing
 CC between, or among, colorectal cell proliferative disorders. The method
 CC involves contacting genomic DNA of a biological sample obtained from the
 CC subject with one or more reagent(s), or a series of reagents that
 CC distinguishes between methylated and non-methylated CpG dinucleotides
 CC within a target sequence of the genomic DNA. The invention further
 CC comprises: a nucleic acid comprising a sequence of 18 or more contiguous
 CC nucleotides of a treated genomic DNA sequence chosen from any one of 284
 CC fully defined nucleotide sequences, whose sequence listing is not
 CC provided in the specification, and their complementary sequences, where
 CC the contiguous sequence has one or more CpG, TpA, or CpA dinucleotide,
 CC and the treatment is suitable to convert one or more of the unmethylated,
 CC cytosine base(s) of the genomic DNA sequence initially to uracil or
 CC another base that is detectably dissimilar to cytosine in terms of
 CC hybridization; an oligomer or peptide nucleic acid (PNA)-oligomer,
 CC comprising 9 or more contiguous nucleotides that is complementary to or
 CC hybridizes under moderately stringent or stringent conditions to one of
 CC the 284 DNA sequences and their complementary sequences provided in the
 CC source document, which is treated; a set of oligomers comprising two or
 CC more of the oligomer of PNA-oligomer; an array of oligomers; and a kit
 CC for carrying out the above methods. The method and its novel compositions
 CC have cytostatic activity. The polynucleotide sequence may be used in gene
 CC therapy. The above methods are useful for detecting and distinguishing
 CC between, or among, colorectal cell proliferative disorders chosen from
 CC colorectal carcinoma, colon adenomas and colon polyps, in a biological
 CC sample, such as histological slides, biopsies, paraffin embedded tissue,
 CC bodily fluids, stool, blood, serum, plasma and their combinations. The
 CC oligomer array is useful as a probe for detecting one or more of the
 CC cytosine methylation state, or single nucleotide polymorphisms within the
 CC genomic DNA or their complementary sequences. The polynucleotides of the

CC invention are useful for classifying, distinguishing between, or among,
 CC diagnosing or determining the predisposition for colorectal cell
 CC proliferative disorders, or for the therapy of colorectal cell
 CC proliferative disorders. This polynucleotide sequence represents a primer
 CC used in the exemplification of the invention.

XX Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.4e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
 Db 4 GGGCGGC 10

RESULT 691

AD267948
 ID AD267948 standard; DNA; 10 BP.

XX AC AD267948;

XX 14-JUL-2005 (first entry)

XX NTRK1 gene polymorphic site 12 primer extension oligonucleotide.

KW Neurotrophic tyrosine kinase receptor type 1; NTRK1; Alzheimer's disease;
 KW neurological disease; diagnosis; prognosis; primer; SNP detection;
 KW haplotype mapping; ss.

XX Homo sapiens.

XX WO2005037204-A2.

XX 28-APR-2005.

XX 14-OCT-2004; 2004WO-US033689.

XX 15-OCT-2003; 2003US-0511247P.

XX (GENA-) GENAISSANCE PHARM.

PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
 PI Judson RS, Ozdemir V, Reed CR;

XX WPI; 2005-322749/33.

XX Determining whether individual has age of onset marker I or marker II, by
 PT determining whether individual has zero copies or copy of neurotrophic
 PT tyrosine kinase, receptor, type 1 haplotypes involved in onset of
 PT Alzheimer's disease.

XX Disclosure; SEQ ID NO 46; 128pp; English.

XX The inventors have discovered a set of 112 haplotypes in the human
 CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene AD267903 that
 CC are associated with the age of onset of Alzheimer's disease (AD). They
 CC have also discovered that the copy number of each of these NTRK1
 CC haplotypes affects the age of onset of AD. If an individual has at least
 CC one copy of any of the 112 specified haplotypes, that individual is
 CC defined as having an 'age of onset marker I' and is more likely to have a
 CC later age of onset of AD than an individual having zero copies of any of
 CC the 112 haplotypes, such as an individual being defined as 'age of onset
 CC marker II'. Testing for the presence or absence, and copy number, of the
 CC haplotypes is useful for predicting the age at which individuals who are
 CC at increased risk of AD are likely to develop AD and to help confirm a
 CC diagnosis of mild or minimal cognitive impairment (MDI) or AD. Such
 CC knowledge will assist therapy and lifestyle decisions. The correlation of
 CC certain NTRK1 haplotypes with age of AD onset indicates that variation in
 CC the NTRK1 gene should be considered in the development and clinical
 CC trials of drugs for treating MCI, AD and other neurodegenerative
 CC disorders. This correlation also provides a basis for pursuing NTRK1 as a

CC target for drugs designed to treat cognitive disorders such as MDI, AD
 CC and other neurological diseases or conditions. Information is provided
 CC about the composition of each of 112 haplotypes, namely the location in
 CC the NTRK1 gene of each of the polymorphic sites (PSs) and the identity of
 CC the reference and variant allele at each PS. An individual's genotype for
 CC the set of PSs is obtained by primer extension, mismatch detection, enzymatic
 CC nucleic acid amplification, hybridization, mismatch detection, enzymatic
 CC nucleic acid cleavage or sequencing assay. The present sequence is that
 CC of a reverse primer extension oligonucleotide for detecting PS12 in
 CC haplotypes comprising preferred embodiments of age of onset markers I and
 CC II.

XX SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGCGCG 10

Db 2 CGGCGCG 8

RESULT 692

AEA62015
 ID AEA62015 standard; DNA; 10 BP.

XX AC AEA62015;

XX 11-AUG-2005 (first entry)

XX NTRK1 gene polymorphic site 12 primer extension oligonucleotide.

KW NTRK1 gene; neurotrophic tyrosine kinase, receptor, type 1;
 KW Alzheimer's disease; degeneration; neurological disease;
 KW haplotype mapping; prognosis; primer; ss; SNP detection.

XX Homo sapiens.

XX WO2005052180-A2.

XX 09-JUN-2005.

XX 22-NOV-2004; 2004WO-US038876.

XX 24-NOV-2003; 2003US-0524636P.

XX (GENA-) GENAISSANCE PHARM INC.

PI Aerssens J, Athanasiou M, Brain C, Cohen N, Dain B, Denton RR;
 PI Judson RS, Ozdemir V, Reed CR;

XX WPI; 2005-418015/42.

XX Determining whether an individual has a progression marker I or
 PT progression marker II, useful for predicting an individual's progression
 PT of Alzheimer's disease, by determining whether the individual has any of
 PT the NTRK1 haplotypes.

XX Claim 40; SEQ ID NO 56; 108pp; English.

XX The present invention relates to genetic markers of the human
 CC neurotrophic tyrosine kinase, receptor, type 1 (NTRK1) gene AEA61960 that
 CC are associated with progression of Alzheimer's disease (AD). 12
 CC Polymorphic sites (PSs) have been discovered in the NTRK1 gene of
 CC Caucasian individuals with AD, and a set of 70 haplotypes having
 CC association with progression of AD have been identified. If an individual
 CC has 0 or 1 copy of any of haplotypes 1-41 and 67-70, or 0 copies of any
 CC of haplotypes 42-66, then that individual is defined as having a
 CC progression marker I and is more likely to exhibit a slower progression
 CC of AD than an individual having 2 copies of any of haplotypes 1-41 and 67
 CC -70, or at least 1 copy of any of haplotypes 42-66, such as an individual
 CC being defined as having a progression marker II. Additional haplotypes

CC may be identified that are in linkage disequilibrium with any of
 CC haplotypes 1-70, referred to as linked haplotypes and substitute
 CC haplotypes of any of haplotypes 1-70, in which one or more of the pss in
 CC the original haplotype is substituted with another PS, where the allele
 CC at the substituted PS is in linkage disequilibrium with the allele at the
 CC substituting PS. The invention provides methods and kits for determining
 CC whether an individual has a progression marker I or a progression marker
 CC II. A method is also provided for predicting an individual's progression
 CC of AD. The individual is especially a Caucasian diagnosed as having a
 CC cognitive disorder. An individual's genotype for each PS may be obtained
 CC by primer extension, allele-specific PCR, nucleic acid amplification,
 CC hybridization, mismatch-detection, enzymatic nucleic acid cleavage or
 CC sequencing assay. The present sequence is a reverse primer extension
 CC oligonucleotide that can be used to detect the allele at PS12 of the
 CC NTRK1 gene. The 3' terminus of the oligonucleotide is complementary to
 CC the nucleotide located immediately adjacent to the PS. The
 CC oligonucleotide is included in a claimed kit of the invention used to
 CC determine whether an individual has a progression marker I or progression
 CC marker II.

XX SQ Sequence 10 BP; 2 A; 3 C; 5 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGGCGG 10

Db 2 CGGCGG 8

|||||

RESULT 693

AEA52329

ID AEA52329 standard; DNA; 10 BP.

XX AC AEA52329;

XX DT 25-AUG-2005 (first entry)

XX DE Prostate cancer gene PCR primer SEQ ID NO 932.

XX KW gene expression; cell proliferation; hyperproliferation; cytostatic;

XX KW neoplasm; PCR; primer; ss.

XX OS Homo sapiens.

XX PN WO2005054517-A2.

XX PD 16-JUN-2005.

XX PF 01-DEC-2004; 2004WO-US040289.

XX PR 01-DEC-2003; 2003EP-00090414.

XX PR 10-FEB-2004; 2004EP-00090404.

XX PR 10-MAY-2004; 2004EP-00090187.

XX PR 21-JUL-2004; 2004EP-00090292.

XX PA (EPIG-) EPIGENOMICS AG.

XX PI Day KJ, Cottrell S, Distler J, Morotti A, Yamamura S, Dekker S;

XX PI Ocamp Y, Devos T;

XX DR WPI; 2005-425434/43.

XX PT Detecting and/or differentiating prostate cell proliferative disorders in
 XX PT a subject by contacting genomic with reagent(s) that distinguishes
 XX PT between methylated and non-methylated CpG dinucleotides in target nucleic
 XX PT acids.

XX PS Example 1; SEQ ID NO 932; 164pp; English.

XX PS The invention describes a method of detecting and/or differentiating
 CC between prostate cell proliferative disorders in a subject comprising

CC contacting genomic DNA isolated from a biological sample with at least
 CC one reagent, or series of reagents that distinguishes between methylated
 CC and non-methylated CpG dinucleotides within one or a combination of
 CC target nucleic acids e.g. HISTONE H4. Also described are: a treated
 CC nucleic acid derived from SEQ ID NO: 1-59, 1017-1028, 1116, 1171, where
 CC the treatment converts at least one unmethylated cytosine base of the
 CC genomic DNA sequence to uracil or another base that is detectable
 CC dissimilar to cytosine in terms of hybridization; a nucleic acid
 CC comprising at least 16 contiguous nucleotides of a treated genomic DNA
 CC sequence selected from SEQ ID NO: 60-295, 1029-1076, 1117-1120, 1172-1175
 CC and sequences complementary to them; an oligomer comprising a sequence of
 CC at least 9 contiguous nucleotides that is complementary to, or hybridizes
 CC under moderately stringent or stringent conditions to a treated genomic
 CC DNA sequence above; a set of oligomers comprising at least two
 CC oligonucleotides as above; and a kit useful for detecting and/or
 CC distinguishing between or among prostate cell proliferative disorder of a
 CC subject comprising at least one of a bisulfite reagent, or a methylation-
 CC sensitive restriction enzyme, and at least one nucleic acid molecule or
 CC peptide nucleic acid molecule comprising a contiguous sequence at least 9
 CC nucleotides that is complementary to, or hybridizes under moderately
 CC stringent or stringent conditions to a sequence selected from SEQ ID NO:
 CC 60-295, 1029-1076, 1117-1120, 1172-1175 and their complements. The
 CC method, nucleic acid, oligomer, set of oligonucleotide, and kit are
 CC useful for detecting and/or differentiating between or among cell
 CC proliferative disorders. This sequence represents a primer used to
 CC analyze methylation status of genes encoding a prostate cell
 CC proliferation associated protein.

XX SQ Sequence 10 BP; 0 A; 3 C; 7 G; 0 T; 0 U; 0 Other;

Query Match 43.8%; Score 7; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 3.4e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11

Db 4 GGGCGGC 10

|||||

Search completed: May 9, 2006, 16:45:22

Job time : 1 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:47:24 ; Search time 1 Seconds
(without alignments)
0.075 Million cell updates/sec

Title: US-09-904-968A-20-COPY

Perfect score: 16

Sequence: 1 cggcggcgccatcgt 16

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 210 seqs, 2342 residues

Total number of hits satisfying chosen parameters: 420

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 211 summaries

Database : pubmaindb20.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	16	1	US-09-904-968A-20
2	12.4	77.5	14	1	US-10-291-230-19
3	12.4	77.5	14	1	US-10-291-249-19
4	11.4	71.2	16	1	US-10-712-672-1460
5	11.4	71.2	16	1	US-10-712-672-1461
6	10.8	67.5	14	1	US-09-093-972C-695
7	10.8	67.5	14	1	US-10-758-451-695
8	10.8	67.5	15	1	US-09-093-972C-673
9	10.8	67.5	15	1	US-09-093-972C-694
10	10.8	67.5	15	1	US-10-758-451-673
11	10.8	67.5	15	1	US-10-758-451-694
12	10.4	65.0	12	1	US-09-093-972C-697
13	10.4	65.0	12	1	US-10-758-451-697
14	10.4	65.0	13	1	US-09-093-972C-675
15	10.4	65.0	13	1	US-09-093-972C-696
16	10.4	65.0	13	1	US-10-758-451-675
17	10.4	65.0	13	1	US-10-758-451-696
18	10.4	65.0	14	1	US-09-093-972C-652
19	10.4	65.0	14	1	US-09-093-972C-674
20	10.4	65.0	14	1	US-10-758-451-652
21	10.4	65.0	14	1	US-10-758-451-674
22	10	62.5	10	1	US-10-487-934-312
23	10	62.5	13	1	US-10-091-281-458
24	10	62.5	13	1	US-10-257-017B-100005
25	10	62.5	13	1	US-10-257-017B-100006
26	10	62.5	13	1	US-10-257-017B-229445
27	10	62.5	13	1	US-10-257-017B-229446
28	10	62.5	13	1	US-10-257-017B-229447
29	10	62.5	13	1	US-10-257-017B-229448
30	9.8	61.2	13	1	US-09-093-972C-716
31	9.8	61.2	13	1	US-10-758-451-716
32	9.8	61.3	14	1	US-09-504-231A-1425
33	9.8	61.3	14	1	US-09-274-553D-1425

34	9.8	61.2	14	1	US-09-093-972C-715	Sequence 715, App
35	9.8	61.2	14	1	US-10-758-451-715	Sequence 715, App
36	9.4	58.7	11	1	US-09-093-972C-698	Sequence 698, App
37	9.4	58.7	11	1	US-09-093-972C-718	Sequence 718, App
38	9.4	58.7	11	1	US-09-093-972C-755	Sequence 755, App
39	9.4	58.7	11	1	US-10-758-451-698	Sequence 698, App
40	9.4	58.7	11	1	US-10-758-451-718	Sequence 718, App
41	9.4	58.7	11	1	US-10-758-451-755	Sequence 755, App
42	9.4	58.7	12	1	US-09-093-972C-676	Sequence 676, App
43	9.4	58.7	12	1	US-09-093-972C-717	Sequence 717, App
44	9.4	58.7	12	1	US-09-093-972C-736	Sequence 736, App
45	9.4	58.7	12	1	US-09-093-972C-754	Sequence 754, App
46	9.4	58.7	12	1	US-10-758-451-676	Sequence 676, App
47	9.4	58.7	12	1	US-10-758-451-717	Sequence 717, App
48	9.4	58.7	12	1	US-10-758-451-736	Sequence 736, App
49	9.4	58.7	12	1	US-10-758-451-754	Sequence 754, App
50	9.4	58.7	13	1	US-09-093-972C-653	Sequence 653, App
51	9.4	58.7	13	1	US-09-093-972C-735	Sequence 735, App
52	9.4	58.7	13	1	US-09-093-972C-753	Sequence 753, App
53	9.4	58.7	13	1	US-10-257-017B-227179	Sequence 227179, App
54	9.4	58.7	13	1	US-10-257-017B-227180	Sequence 227180, App
55	9.4	58.7	13	1	US-10-758-451-653	Sequence 653, App
56	9.4	58.7	13	1	US-10-758-451-735	Sequence 735, App
57	9.4	58.7	13	1	US-10-758-451-753	Sequence 753, App
58	9	56.2	10	1	US-09-093-972C-738	Sequence 738, App
59	9	56.2	10	1	US-09-093-972C-756	Sequence 756, App
60	9	56.2	10	1	US-10-758-451-738	Sequence 738, App
61	9	56.2	10	1	US-10-758-451-756	Sequence 756, App
62	9	56.2	11	1	US-09-093-972C-737	Sequence 737, App
63	9	56.2	11	1	US-10-758-451-737	Sequence 737, App
64	9	56.2	12	1	US-09-739-068-13	Sequence 13, Appl
65	9	56.2	12	1	US-10-091-281-459	Sequence 459, App
66	9	56.2	12	1	US-10-257-017B-269661	Sequence 269661, App
67	9	56.2	12	1	US-10-257-017B-289845	Sequence 289845, App
68	9	56.2	12	1	US-10-257-017B-322850	Sequence 322850, App
69	9	56.2	12	1	US-10-257-017B-322854	Sequence 322854, App
70	9	56.2	12	1	US-10-257-017B-322858	Sequence 322858, App
71	9	56.2	12	1	US-10-257-017B-299697	Sequence 299697, App
72	8.8	55.0	12	1	US-10-257-017B-311797	Sequence 311797, App
73	8.8	55.0	12	1	US-09-093-972C-699	Sequence 699, App
74	8.4	52.5	10	1	US-09-093-972C-719	Sequence 719, App
75	8.4	52.5	10	1	US-09-093-972C-773	Sequence 773, App
76	8.4	52.5	10	1	US-10-113-877-39	Sequence 39, Appl
77	8.4	52.5	10	1	US-10-146-354A-4	Sequence 4, Appl
78	8.4	52.5	10	1	US-10-356-792-27	Sequence 27, Appl
79	8.4	52.5	10	1	US-10-602-494-366	Sequence 366, App
80	8.4	52.5	10	1	US-10-758-451-699	Sequence 699, App
81	8.4	52.5	10	1	US-10-758-451-719	Sequence 719, App
82	8.4	52.5	10	1	US-10-758-451-773	Sequence 773, App
83	8.4	52.5	11	1	US-08-944-410-79	Sequence 79, Appl
84	8.4	52.5	11	1	US-09-974-143A-10	Sequence 10, Appl
85	8.4	52.5	11	1	US-09-093-972C-677	Sequence 677, App
86	8.4	52.5	11	1	US-09-093-972C-772	Sequence 772, App
87	8.4	52.5	11	1	US-10-112-267-44	Sequence 44, Appl
88	8.4	52.5	11	1	US-10-214-417A-45	Sequence 45, Appl
89	8.4	52.5	11	1	US-10-434-588-41	Sequence 41, Appl
90	8.4	52.5	11	1	US-10-628-770-24	Sequence 24, Appl
91	8.4	52.5	11	1	US-10-659-549-23	Sequence 23, Appl
92	8.4	52.5	11	1	US-10-758-451-677	Sequence 677, App
93	8.4	52.5	11	1	US-10-758-451-772	Sequence 772, App
94	8.4	52.5	11	1	US-09-093-972C-654	Sequence 654, App
95	8.4	52.5	12	1	US-10-096-718-7	Sequence 7, Appl
96	8.4	52.5	12	1	US-10-096-718-27	Sequence 27, Appl
97	8.4	52.5	12	1	US-10-670-011-387	Sequence 387, App
98	8.4	52.5	12	1	US-10-257-017B-277600	Sequence 277600, App
99	8.4	52.5	12	1	US-10-257-017B-314171	Sequence 314171, App
100	8.4	52.5	12	1	US-10-257-017B-322459	Sequence 322459, App
101	8.4	52.5	12	1	US-10-764-957-387	Sequence 387, App

[illegible]

RESULT 2
US-10-291-230-19/c
; Sequence 19, Application US/10291230
; Publication No. US20030108939A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 US.A
; CURRENT APPLICATION NUMBER: US/10/291,230
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-230-19

Query Match 77.5%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCATCG 1

RESULT 3
US-10-291-249-19/c
; Sequence 19, Application US/10291249
; Publication No. US20030119041A1
; GENERAL INFORMATION:
; APPLICANT: Ruffner, Duane E.
; APPLICANT: Pierce, Michael L.
; APPLICANT: Chen, Zhidong
; TITLE OF INVENTION: Directed Antisense Libraries
; FILE REFERENCE: T6678 US.B
; CURRENT APPLICATION NUMBER: US/10/291,249
; CURRENT FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 09/647,344
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: PCT/US99/06742
; PRIOR FILING DATE: 1999-03-28
; PRIOR APPLICATION NUMBER: US 60/079,792
; PRIOR FILING DATE: 1998-03-28
; PRIOR APPLICATION NUMBER: US 60/107,504
; PRIOR FILING DATE: 1998-11-06
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 14
; TYPE: DNA
; ORGANISM: herpes simplex virus
US-10-291-249-19

Query Match 77.5%; Score 12.4; DB 1; Length 14;
Best Local Similarity 92.9%; Pred. No. 10;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCATCG 1

RESULT 4
US-10-712-672-1460/c
; Sequence 1460, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1460
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1460

Query Match 71.2%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
||| ||||| |||
Db 16 GCGGGCGGCATCG 4

RESULT 5
US-10-712-672-1461/c
; Sequence 1461, Application US/10712672
; Publication No. US20040102413A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Chowrira, Bharat
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: Method and Reagent for the Inhibition of Telomerase Enzyme
; FILE REFERENCE: MHB00-882-C (400/019)
; CURRENT APPLICATION NUMBER: US/10/712,672
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US/09/653,225
; PRIOR FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/197,769
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/150,713
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 5586
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1461
; LENGTH: 16
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-712-672-1461

Query Match 71.2%; Score 11.4; DB 1; Length 16;
Best Local Similarity 92.3%; Pred. No. 21;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCATCG 15
||| ||||| |||
Db 14 GCGGGCGGCATCG 2

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RESULT 6
US-09-093-972C-695
; Sequence 695, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-June-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 695:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 695:
US-09-093-972C-695

Query Match 67.5%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
Db 1 GGAGGGCGGCATGG 14

RESULT 7
US-10-758-451-695
; Sequence 695, Application US/10758451
; Publication No. US2005001471A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF B
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
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; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 695
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-758-451-695

Query Match 67.5%; Score 10.8; DB 1; Length 14;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCATCG 15
Db 1 GGAGGGCGGCATGG 14

RESULT 8
US-09-093-972C-673
; Sequence 673, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-June-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 673:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 673:
US-09-093-972C-673
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Query Match      67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCATCG 15
   ||| ||||| |||
Db 2 GGAGGGCGGCATGG 15

RESULT 9
US-09-093-972C-694
; Sequence 694, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093.972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION DATA:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 694:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 694:

US-09-093-972C-694

Query Match      67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCATCG 15
   ||| ||||| |||
Db 1 GGAGGGCGGCATGG 14

RESULT 10
US-10-758-451-673
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; Sequence 673, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 673
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-758-451-673

Query Match      67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCATCG 15
   ||| ||||| |||
Db 2 GGAGGGCGGCATGG 15

RESULT 11
US-10-758-451-694
; Sequence 694, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 694
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-758-451-694

Query Match      67.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 27;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCATCG 15
   ||| ||||| |||
Db 1 GGAGGGCGGCATGG 14

RESULT 12
US-09-093-972C-697
; Sequence 697, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
```

```
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 697:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 697:
US-09-093-972C-697
Query Match 65.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 23;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 1 GGAGGGCGGCAT 12

RESULT 13
US-10-758-451-697
; Sequence 697, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 697
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-697
Query Match 65.0%; Score 10.4; DB 1; Length 12;
Best Local Similarity 91.7%; Pred. No. 23;

; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 697:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 697:
US-09-093-972C-697
Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 1 GGAGGGCGGCAT 12

RESULT 14
US-09-093-972C-675
; Sequence 675, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; TITLE OF INVENTION: & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; TITLE OF INVENTION: BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 675:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 675:
US-09-093-972C-675
Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGCAT 13
Db 2 GGAGGGCGGCAT 13

RESULT 15
US-09-093-972C-696
; Sequence 696, Application US/09093972C
; Publication No. US20030087845A1
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; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 696:
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 696:
US-09-093-972C-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
|| |||||
Db 1 GGAGGGCGGCAT 12

RESULT 16
US-10-758-451-675
; Sequence 675, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 696
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-758-451-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
|| |||||
Db 1 GGAGGGCGGCAT 12

RESULT 17
US-10-758-451-696
; Sequence 696, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 696
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-758-451-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
|| |||||
Db 2 GGAGGGCGGCAT 13

RESULT 18
US-09-093-972C-652
; Sequence 652, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 675
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-758-451-675

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
|| |||||
Db 2 GGAGGGCGGCAT 13

RESULT 17
US-10-758-451-696
; Sequence 696, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 696
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; ORGANISM: Homo sapiens
US-10-758-451-696

Query Match 65.0%; Score 10.4; DB 1; Length 13;
Best Local Similarity 91.7%; Pred. No. 26;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
|| |||||
Db 1 GGAGGGCGGCAT 12

RESULT 18
US-09-093-972C-652
; Sequence 652, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
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; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-674

Query Match 65.0%; Score 10.4; DB 1; Length 14;
Best Local Similarity 91.7%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCAT 13
||| |||||
Db 2 GGAGGCGGCAT 13

RESULT 22

US-10-487-934-312/c
; Sequence 312, Application US/10487934
; Publication No. US20040265824A1
; GENERAL INFORMATION:
; APPLICANT: Buckhaults, Phillip
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: EXPRESSED AND CELL SURFACE GENES
; TITLE OF INVENTION: EXPRESSED IN BENIGN AND MALIGNANT COLORECTAL TUMORS
; FILE REFERENCE: 001107.00429
; CURRENT APPLICATION NUMBER: US/10/487,934
; CURRENT FILING DATE: 2004-03-03
; PRIOR APPLICATION NUMBER: 60/317,494
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/383,805
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 312
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-487-934-312

Query Match 62.5%; Score 10; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCA 12
||| |||||
Db 10 GCGGGCGGCA 1

RESULT 23

US-10-091-281-458
; Sequence 458, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587,338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 458
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative SP1F/SP1.01 motif
US-10-091-281-458

Query Match 62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGCGGC 11
||| |||||
Db 1 GCGGGCGGC 10

RESULT 24

US-10-257-017B-100005
; Sequence 100005, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100005
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024859
US-10-257-017B-100005

Query Match 62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGCGGC 11
||| |||||
Db 1 GCGGGCGGC 10

RESULT 25

US-10-257-017B-100006/c
; Sequence 100006, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 100006
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0024859
US-10-257-017B-100006

Query Match 62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGCGGC 11
||| |||||
Db 13 GCGGGCGGC 4

RESULT 26

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US-10-257-017B-229445
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; PUBLICATION NO. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229445
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229445

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGG 10
Db 4 CGCGCGGCGG 13

RESULT 27
US-10-257-017B-229446/c
; Sequence 229446, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229446
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229446

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGG 10
Db 10 CGCGCGGCGG 1

RESULT 28
US-10-257-017B-229447
; Sequence 229447, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
```

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; PUBLICATION NO. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229447
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229447

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGG 10
Db 4 CGCGCGGCGG 13

RESULT 29
US-10-257-017B-229448/c
; Sequence 229448, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 229448
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for detection of SNP TSC0055973
US-10-257-017B-229448

Query Match      62.5%; Score 10; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGG 10
Db 10 CGCGCGGCGG 1

RESULT 30
US-09-093-972C-716
; Sequence 716, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
```

;; COUNTRY: USA
;; ZIP: 08512
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/093,972C
;; FILING DATE: 09-Jun-1998
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/472,527
;; FILING DATE: 7-June-1995
;; APPLICATION NUMBER: US 08/757,024
;; FILING DATE: 26-11-1996
;; APPLICATION NUMBER: US 08/472,527
;; FILING DATE: 7-June-1995
;; APPLICATION NUMBER: US 09/016,464
;; FILING DATE: 30-January-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amzel, Viviana
;; REGISTRATION NUMBER: 30,930
;; REFERENCE/DOCKET NUMBER: EPI-00672
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-409-3035
;; TELEFAX: 413-254-9245
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 716:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 716:
US-09-093-972C-716

Query Match 61.2%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCATCG 15
| | | | | | | | | |
Db 1 GAGGGCGGCATGG 13

RESULT 31
US-10-758-451-716
; Sequence 716, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 716
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-716

Query Match 61.2%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 36;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCATCG 15
| | | | | | | | | |
Db 1 GAGGGCGGCATGG 13

RESULT 32
US-09-504-231A-1425/c
; Sequence 1425, Application US/09504231A
; Patent No. US20020013458A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/504,231A
; CURRENT FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: 09/274,553
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3242
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1425
; LENGTH: 14
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-504-231A-1425

Query Match 61.3%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.8%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGGGCGGGCGGCAT 13
| | | | | | | | | |
Db 13 CGCGGAGCTGCAT 1

RESULT 33
US-09-274-553D-1425/c
; Sequence 1425, Application US/09274553D
; Patent No. US2002008225A1
; GENERAL INFORMATION:
; APPLICANT: Blatt, Lawrence
; APPLICANT: McSwiggen, James
; APPLICANT: Roberts, Beth
; APPLICANT: Pavco, Pamela
; APPLICANT: Macejak, Dennis
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT OF DISEASES OR CONDITIONS RELAT
; TITLE OF INVENTION: HEPATITIS C VIRUS INFECTION
; FILE REFERENCE: IPI 247/282
; CURRENT APPLICATION NUMBER: US/09/274,553D
; CURRENT FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 09/257,608
; PRIOR FILING DATE: 1999-02-24
; PRIOR APPLICATION NUMBER: 60/100,842
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/083,217
; PRIOR FILING DATE: 1998-04-27
; NUMBER OF SEQ ID NOS: 3148
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1425
; LENGTH: 14
; TYPE: RNA

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Nucleic Acid Target
US-09-274-553D-1425

Query Match          61.3%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 CGCGCGGCGGCAT 13
        ||||| |||||
Db       13 CGCGGAGCTGCAT 1

RESULT 34
US-09-093-972C-715
; Sequence 715, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:
US-09-093-972C-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCGGGCGGCATCG 15
        ||||| |||||
```

```
Db       1 GAGGGCGGCATCG 13

RESULT 35
US-10-758-451-715
; Sequence 715, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 715
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCGGGCGGCATCG 15
        ||||| |||||
Db       1 GAGGGCGGCATCG 13

RESULT 36
US-09-093-972C-698
; Sequence 698, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELE: <Unknown>
; INFORMATION FOR SEQ ID NO: 715:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 715:
US-09-093-972C-715

Query Match          61.2%; Score 9.8; DB 1; Length 14;
Best Local Similarity 84.6%; Pred. No. 40;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 GCGGGCGGCATCG 15
        ||||| |||||
```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 698:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 698:
US-09-093-972C-698

Query Match 58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGCGCGCA 12
| | | | | | | |
Db 1 GGAGGCGGCA 11

RESULT 37

US-09-093-972C-718
; Sequence 718, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.

; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Anzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 718:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 718:
US-09-093-972C-718

Query Match 58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGCGCGCAT 13
| | | | | | | |
Db 1 GAGGCGCGCAT 11

RESULT 38

US-09-093-972C-755
; Sequence 755, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.

; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 755:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 755:
US-09-093-972C-755

Query Match 58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGGCGCGCATG 15
| | | | | | | |
Db 1 GGCGCGCATGG 11

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RESULT 39
US-10-758-451-698
; Sequence 698, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 698
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-698

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGCA 12
   ||| |||||
Db 1 GGAGGGCGGCA 11

RESULT 40
US-10-758-451-718
; Sequence 718, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 718
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-718

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCAT 13
   ||| |||||
Db 1 GAGGGCGGCAT 11

RESULT 41
US-10-758-451-755
; Sequence 755, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
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; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 755
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-755

Query Match      58.7%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 35;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
   ||| |||||
Db 1 GGGCGGCATGG 11

RESULT 42
US-09-093-972C-676
; Sequence 676, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: NYce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSER: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 676:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 676:
US-09-093-972C-676
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Query Match 58.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 40;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGCA 12
 |||||
 Db 2 GGAGGGCGCA 12
 |||||

RESULT 43
 US-09-093-972C-717
 ; Sequence 717, Application US/09093972C
 ; Publication No. US20030087845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 08512
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/093,972C
 ; FILING DATE: 09-Jun-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 08/757,024
 ; FILING DATE: 26-11-1996
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 09/016,464
 ; FILING DATE: 30-January-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel, Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: EPI-00672
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-409-3035
 ; TELEFAX: 413-254-9245
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 717:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 717:

Query Match 58.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 40;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GCGGGCGGCAT 13
 |||||
 Db 1 GAGGGCGCAT 11
 |||||

RESULT 44

US-09-093-972C-736
 ; Sequence 736, Application US/09093972C
 ; Publication No. US20030087845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
 ; STREET: 7 Clarke Drive
 ; CITY: Cranbury
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 08512
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/093,972C
 ; FILING DATE: 09-Jun-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 08/757,024
 ; FILING DATE: 26-11-1996
 ; APPLICATION NUMBER: US 08/472,527
 ; FILING DATE: 7-June-1995
 ; APPLICATION NUMBER: US 09/016,464
 ; FILING DATE: 30-January-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Amzel, Viviana
 ; REGISTRATION NUMBER: 30,930
 ; REFERENCE/DOCKET NUMBER: EPI-00672
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 609-409-3035
 ; TELEFAX: 413-254-9245
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 736:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 12 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 736:

Query Match 58.7%; Score 9.4; DB 1; Length 12;
 Best Local Similarity 90.9%; Pred. No. 40;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCGGGCGCATCG 15
 |||||
 Db 2 GGCGGGCATGG 12
 |||||

RESULT 45

US-09-093-972C-754
 ; Sequence 754, Application US/09093972C
 ; Publication No. US20030087845A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Nyce, Jonathan W.
 ; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
 ; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
 ; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
 ;
 ; NUMBER OF SEQUENCES: 996
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

```

; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 754:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 754:
US-09-093-972C-754

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
| | | | | | |
Db 1 GGGCGGCATGG 11

RESULT 46
US-10-758-451-676
; Sequence 676, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 676
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-676

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
| | | | | | |
Db 1 GGGCGGCATGG 11

RESULT 46
US-10-758-451-676
; Sequence 676, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 676
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-676

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
| | | | | | |
Db 2 GGGCGGCATGG 12

RESULT 49
US-10-758-451-754
; Sequence 754, Application US/10758451
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Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGGCGGCATCG 12
| | | | | | |
Db 2 GGGCGGCATCG 12

RESULT 47
US-10-758-451-717
; Sequence 717, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 717
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-717

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GGGCGGCATCG 13
| | | | | | |
Db 1 GAGGGCGCAT 11

RESULT 48
US-10-758-451-736
; Sequence 736, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 736
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-736

Query Match 58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GGGCGGCATCG 15
| | | | | | |
Db 2 GGGCGGCATGG 12

RESULT 49
US-10-758-451-754
; Sequence 754, Application US/10758451
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```
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758.451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 754
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-754

Query Match      58.7%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      5 GGGCGGCATCG 15
Db      1 GGGCGGCATGG 11
      |||||
      |||||

RESULT 50
US-09-093-972C-653
; Sequence 653, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 653:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 653:
US-09-093-972C-653

Query Match      58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      2 GGGCGGCGGCA 12
Db      3 GGAGGGCGGCA 13
      |||||
      |||||

RESULT 51
US-09-093-972C-735
; Sequence 735, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 735:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 735:
US-09-093-972C-735

Query Match      58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```

Qy 5 GGGCGGCATCG 15
    |||||
Db 2 GGGCGGCATCG 12

RESULT 52
US-09-093-972C-753
; Sequence 753, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-006672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 753:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 753:
;
; US-09-093-972C-753
;
; Query Match 58.7%; Score 9.4; DB 1; Length 13;
; Best Local Similarity 90.9%; Pred. No. 44;
; Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCATCG 15
    |||||
Db 1 GGGCGGCATCG 11

RESULT 53
US-10-257-017B-227179
; Sequence 227179, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:

```

;; PRIOR APPLICATION NUMBER: 09/093,972
;; PRIOR FILING DATE: 1998-06-09
;; NUMBER OF SEQ ID NOS: 996
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 653
;; LENGTH: 13
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-758-451-653

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGGCGGCGGCA 12
||| |||||
Db 3 GGGCGGCGGCA 13

RESULT 56

US-10-758-451-735
;; Sequence 735, Application US/10758451
;; Publication No. US20050014711A1
;; GENERAL INFORMATION:
;; APPLICANT: East Carolina University
;; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
;; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
;; TITLE OF INVENTION: INFLAMMATION
;; FILE REFERENCE: 30775-706.301
;; CURRENT APPLICATION NUMBER: US/10758,451
;; CURRENT FILING DATE: 2004-01-14
;; PRIOR APPLICATION NUMBER: 09/093,972
;; PRIOR FILING DATE: 1998-06-09
;; NUMBER OF SEQ ID NOS: 996
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 735
;; LENGTH: 13
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-758-451-735

Query Match 58.7%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCGATCG 15
||| |||||
Db 2 GGGCGGCGATCG 12

RESULT 57

US-10-758-451-753
;; Sequence 753, Application US/10758451
;; Publication No. US20050014711A1
;; GENERAL INFORMATION:
;; APPLICANT: East Carolina University
;; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
;; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
;; TITLE OF INVENTION: INFLAMMATION
;; FILE REFERENCE: 30775-706.301
;; CURRENT APPLICATION NUMBER: US/10758,451
;; CURRENT FILING DATE: 2004-01-14
;; PRIOR APPLICATION NUMBER: 09/093,972
;; PRIOR FILING DATE: 1998-06-09
;; NUMBER OF SEQ ID NOS: 996
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 753
;; LENGTH: 13
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-758-451-753

Query Match 58.7%; Score 9.4; DB 1; Length 13;

Best Local Similarity 90.9%; Pred. No. 44;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GGGCGGCGATCG 15
||| |||||
Db 1 GGGCGGCGATCG 11

RESULT 58

US-09-093-972C-738
;; Sequence 738, Application US/09093972C
;; Publication No. US20030087845A1
;; GENERAL INFORMATION:
;; APPLICANT: Nyce, Jonathan W.
;; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
;; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
;; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
;; NUMBER OF SEQUENCES: 996
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
;; STREET: 7 Clarke Drive
;; CITY: Cranbury
;; STATE: New Jersey
;; COUNTRY: USA
;; ZIP: 08512
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/093,972C
;; FILING DATE: 09-Jun-1998
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/472,527
;; FILING DATE: 7-June-1995
;; APPLICATION NUMBER: US 08/757,024
;; FILING DATE: 26-11-1996
;; APPLICATION NUMBER: US 08/472,527
;; FILING DATE: 7-June-1995
;; APPLICATION NUMBER: US 09/016,464
;; FILING DATE: 30-January-1998
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Amzel, Viviana
;; REGISTRATION NUMBER: 30,930
;; REFERENCE/DOCKET NUMBER: EPI-00672
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 609-409-3035
;; TELEFAX: 413-254-9245
;; TELEX: <Unknown>
;; INFORMATION FOR SEQ ID NO: 738:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; SEQUENCE DESCRIPTION: SEQ ID NO: 738:

US-09-093-972C-738

Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGCGAT 13
||| |||||
Db 2 GGGCGGCGAT 10

RESULT 59

US-09-093-972C-756
;; Sequence 756, Application US/09093972C

```
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US 09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 756:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 756:
US-09-093-972C-756

Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCAT 13
Db 1 GGGCGGCAT 9

RESULT 60
US-10-758-451-738
; Sequence 738, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
```

```
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 738
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-738

Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCAT 13
Db 2 GGGCGGCAT 10

RESULT 61
US-10-758-451-756
; Sequence 756, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY(IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 756
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-756

Query Match 56.2%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGCAT 13
Db 1 GGGCGGCAT 9

RESULT 62
US-09-093-972C-737
; Sequence 737, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
```

```

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 737:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 737:
US-09-093-972C-737
```

```

Query Match      56.2%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GGGGGGCAT 13
        |||||
Db       2 GGGGGGCAT 10
```

RESULT 63

```

US-10-758-451-737
; Sequence 737, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 737
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-737
```

```

Query Match      56.2%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 GGGGGGCAT 13
        |||||
Db       2 GGGGGGCAT 10
```

RESULT 64

```

US-09-739-068-13
; Sequence 13, Application US/09739068
; Patent No. US20020142297A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Bogdanov, Alexei A.
; Weissleder, Ralph
; Simonova, Maria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR IMAGING
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/739,068
; FILING DATE: 18-Dec-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,366B
; FILING DATE: 29-JAN-1998
; APPLICATION NUMBER: 60/037,350
; FILING DATE: 31-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Fassee, Peter J.
; REGISTRATION NUMBER: 32,983
; REFERENCE/DOCKET NUMBER: 00786/388002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-739-068-13
```

```

Query Match      56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 GGGGGGGCGG 10
        |||||
Db       2 GGGGGGGCGG 10
```

RESULT 65

```

US-10-091-281-459/c
; Sequence 459, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AP2F/AP2.01 motif
US-10-091-281-459
```

```
Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGCG 9
Db 9 CGCGGGGCG 1

RESULT 66
US-10-257-017B-269661/c
; Sequence 269661, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 269661
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0001842
US-10-257-017B-269661

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGCGG 10
Db 11 GCGGGGCGG 3

RESULT 67
US-10-257-017B-289845/c
; Sequence 289845, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 289845
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0014116
US-10-257-017B-289845

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGCG 9
Db 11 CGCGGGGCG 3

RESULT 68
US-10-257-017B-322850
; Sequence 322850, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322850
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322850

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGCG 9
Db 3 CGCGGGGCG 11

RESULT 69
US-10-257-017B-322854
; Sequence 322854, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; PRIOR FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322854
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322854

Query Match          56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGGCG 9
Db 3 CGCGGGGCG 11

RESULT 70
US-10-257-017B-322858
; Sequence 322858, Application US/10257017B
; Publication No. US20040241651A1
```



```

; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322858
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322858

Query Match      56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGGCG 9
Db 3 CGCGGGGCG 11

RESULT 71
US-10-257-017B-322859
; Sequence 322859, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322859
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0031084
US-10-257-017B-322859

Query Match      56.2%; Score 9; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGGCG 9
Db 3 CGCGGGGCG 11

RESULT 72
US-10-257-017B-299697/c
; Sequence 299697, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO

```

```

; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 299697
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0018689
US-10-257-017B-299697

Query Match      55.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GGCGGGCATCGT 16
Db 12 GGCGGGCATCGT 1

RESULT 73
US-10-257-017B-311797
; Sequence 311797, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 311797
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0024693
US-10-257-017B-311797

Query Match      55.0%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 54;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GGCGGGGGCAT 13
Db 1 GGCGGGGGCAT 12

RESULT 74
US-09-093-972C-699
; Sequence 699, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:

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/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/093,972C
/ FILING DATE: 09-Jun-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995
/ APPLICATION NUMBER: US 08/757,024
/ FILING DATE: 26-11-1996
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995
/ APPLICATION NUMBER: US 09/016,464
/ FILING DATE: 30-January-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Amzel, Viviana
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: EPI-00672
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-409-3035
/ TELEFAX: 413-254-9245
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 699:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 699:
US-09-093-972C-699

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGGGCGC 11
DB 1 GGAGGGGGCGC 10

RESULT 75
US-09-093-972C-719
/ Sequence 719, Application US/09093972C
/ Publication No. US20030087845A1
/ GENERAL INFORMATION:
/ APPLICANT: Nyce, Jonathan W.
/ TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
/ & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
/ BRONCHOCOINSTRUCTION, ALLERGY(IES) & INFLAMMATION
/ NUMBER OF SEQUENCES: 996
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
/ STREET: 7 Clarke Drive
/ CITY: Cranbury
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 08512
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/093,972C
/ FILING DATE: 09-Jun-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995

/ APPLICATION NUMBER: US 08/757,024
/ FILING DATE: 26-11-1996
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995
/ APPLICATION NUMBER: US 09/016,464
/ FILING DATE: 30-January-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Amzel, Viviana
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: EPI-00672
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 609-409-3035
/ TELEFAX: 413-254-9245
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 719:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 719:
US-09-093-972C-719

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGGGCGC 12
DB 1 GAGGGGGCGC 10

RESULT 76
US-09-093-972C-773
/ Sequence 773, Application US/09093972C
/ Publication No. US20030087845A1
/ GENERAL INFORMATION:
/ APPLICANT: Nyce, Jonathan W.
/ TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
/ & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
/ BRONCHOCOINSTRUCTION, ALLERGY(IES) & INFLAMMATION
/ NUMBER OF SEQUENCES: 996
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
/ STREET: 7 Clarke Drive
/ CITY: Cranbury
/ STATE: New Jersey
/ COUNTRY: USA
/ ZIP: 08512
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/093,972C
/ FILING DATE: 09-Jun-1998
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995
/ APPLICATION NUMBER: US 08/757,024
/ FILING DATE: 26-11-1996
/ APPLICATION NUMBER: US 08/472,527
/ FILING DATE: 7-June-1995
/ APPLICATION NUMBER: US 09/016,464
/ FILING DATE: 30-January-1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Amzel, Viviana
/ REGISTRATION NUMBER: 30,930
/ REFERENCE/DOCKET NUMBER: EPI-00672
/ TELECOMMUNICATION INFORMATION:

; TELEPHONE: 609-409-3035
 ; TELEFAX: 413-254-9245
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 773:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 773:
 US-09-093-972C-773

Query Match 52.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGCGGCATCG 15
 |||||
 DB 1 GCGCGGCATGG 10

RESULT 77

US-10-113-877-39/c
 ; Sequence 39, Application US/10113877
 ; Publication No. US20020177218A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Yu
 ; APPLICANT: Wang, Xiao-Yang
 ; APPLICANT: Turpin, Pierre
 ; TITLE OF INVENTION: Methods of detecting multiple DNA
 ; TITLE OF INVENTION: Binding protein and DNA interactions in a sample, and
 ; TITLE OF INVENTION: devices, systems and kits for practicing the same.
 ; FILE REFERENCE: CLON-071
 ; CURRENT APPLICATION NUMBER: US/10/113,877
 ; CURRENT FILING DATE: 2002-03-29
 ; PRIOR APPLICATION NUMBER: 60/280,658
 ; PRIOR FILING DATE: 2001-03-30
 ; PRIOR APPLICATION NUMBER: 60/314,330
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 192
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 39
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: oligonucleotide
 US-10-113-877-39

Query Match 52.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCGGCGCG 10
 |||||
 DB 10 CCGCGGCGCG 1

RESULT 78

US-10-146-354A-4
 ; Sequence 4, Application US/10146354A
 ; Publication No. US20030054381A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pfizer Inc.
 ; APPLICANT: Seymour, Albert B.
 ; APPLICANT: Nelson, Darcy L.
 ; APPLICANT: Webb, Suzin M.
 ; APPLICANT: Affourtit, Jason P.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS IN THE HUMAN NEUROKININ 1 RECEPTOR GENE AND
 ; TITLE OF INVENTION: USES IN DIAGNOSIS AND TREATMENT OF DISEASES
 ; FILE REFERENCE: FC10461AGPR
 ; CURRENT APPLICATION NUMBER: US/10/146,354A

; CURRENT FILING DATE: 2002-08-15
 ; PRIOR APPLICATION NUMBER: 60/293,425
 ; NUMBER OF SEQ ID NOS: 48
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-146-354A-4

Query Match 52.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCA 12
 |||||
 DB 1 GCGGACGGCA 10

RESULT 79

US-10-356-792-27/c
 ; Sequence 27, Application US/10356792
 ; Publication No. US20030215842A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sledziwski, Andrzej
 ; APPLICANT: Schweikhardt, Gary
 ; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
 ; FILE REFERENCE: 47675-33
 ; CURRENT APPLICATION NUMBER: US/10/356,792
 ; CURRENT FILING DATE: 2003-01-30
 ; PRIOR APPLICATION NUMBER: 60/352,944
 ; PRIOR FILING DATE: 2002-01-30
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 27
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: artificial sequence
 ; FEATURE:
 ; OTHER INFORMATION: AP-PCR Primer G6
 US-10-356-792-27

Query Match 52.5%; Score 8.4; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 51;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCGGGCGGCAT 13
 |||||
 DB 10 CCGGGCGGCAT 1

RESULT 80

US-10-602-494-366/c
 ; Sequence 366, Application US/10602494
 ; Publication No. US20040265833A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cathy Lofton-Day
 ; APPLICANT: Andrew Sledziwski
 ; APPLICANT: Jeff Thomas
 ; APPLICANT: Robert W. Day
 ; APPLICANT: Lori Tonnes-Priddy
 ; APPLICANT: Karen Cardon
 ; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
 ; TITLE OF INVENTION: proliferative disorders
 ; FILE REFERENCE: 47675-45
 ; CURRENT APPLICATION NUMBER: US/10/602,494
 ; CURRENT FILING DATE: 2003-06-23
 ; NUMBER OF SEQ ID NOS: 385
 ; SEQ ID NO 366
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo Sapiens

US-10-602-494-366

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CGGGCGGCAT 13
|||||||

DB 10 CGGGCGGCAT 1

RESULT 81
US-10-758-451-699
; Sequence 699, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 699
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-699

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGCGGC 11
|||

DB 1 GGAGGGCGGC 10

RESULT 82
US-10-758-451-719
; Sequence 719, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 719
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-719

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGGCGGCA 12
|||||||

DB 1 GAGGGCGGCA 10

RESULT 83
US-10-758-451-773
; Sequence 773, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF I
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 773
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-773

Query Match 52.5%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 51;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGGCATCG 15
|||||||

DB 1 GGCGGCATCG 10

RESULT 84
US-08-944-410-79/c
; Sequence 79, Application US/08944410
; Publication No. US20030050453A1
; GENERAL INFORMATION:
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: COLLECTIONS OF UNIQUELY TAGGED MOLECULES
; FILE REFERENCE: 04121.0018-0000
; CURRENT APPLICATION NUMBER: US/08/944,410
; CURRENT FILING DATE: 1997-10-06
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 79
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic primer
US-08-944-410-79

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGCGGCGG 10
|||||||

DB 11 CGGAGGGCGG 2

RESULT 85
US-09-974-143A-10/c
; Sequence 10, Application US/09974143A
; Publication No. US2003002326A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL FETAL GENES
; FILE REFERENCE: 06501-089001
; CURRENT APPLICATION NUMBER: US/09/974,143A
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: PCT/JP00/02281
; PRIOR FILING DATE: 2000-04-07

;; PRIOR APPLICATION NUMBER: JP 11/103356

;; PRIOR FILING DATE: 1999-04-09

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 4.0

;; SEQ ID NO 10

;; LENGTH: 11

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Artificially synthesized adapter sequence

US-09-974-143A-10

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGCGG 10

Db 11 CGGAGGCGG 2

RESULT 86

US-09-093-972C-677

;; Sequence 677, Application US/09093972C

;; Publication No US20030087845A1

;; GENERAL INFORMATION:

;; APPLICANT: Nyce, Jonathan W.

;; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
;& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION

;; NUMBER OF SEQUENCES: 996

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

;; STREET: 7 Clarke Drive

;; CITY: Cranbury

;; STATE: New Jersey

;; COUNTRY: USA

;; ZIP: 08512

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/093,972C

;; FILING DATE: 09-Jun-1998

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 08/757,024

;; FILING DATE: 26-11-1996

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 09/016,464

;; FILING DATE: 30-January-1998

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Amzel, Viviana

;; REGISTRATION NUMBER: 30,930

;; REFERENCE/DOCKET NUMBER: EPI-00672

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 609-409-3035

;; TELEFAX: 413-254-9245

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 677:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 11 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; SEQUENCE DESCRIPTION: SEQ ID NO: 677:

US-09-093-972C-677

Query Match 52.5%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGGGCGGC 11

Db 2 GGAGGGCGC 11

RESULT 87

US-09-093-972C-772

;; Sequence 772, Application US/09093972C

;; Publication No. US20030087845A1

;; GENERAL INFORMATION:

;; APPLICANT: Nyce, Jonathan W.

;; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
;& TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION

;; NUMBER OF SEQUENCES: 996

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.

;; STREET: 7 Clarke Drive

;; CITY: Cranbury

;; STATE: New Jersey

;; COUNTRY: USA

;; ZIP: 08512

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible

;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/093,972C

;; FILING DATE: 09-Jun-1998

;; CLASSIFICATION: <Unknown>

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 08/757,024

;; FILING DATE: 26-11-1996

;; APPLICATION NUMBER: US 08/472,527

;; FILING DATE: 7-June-1995

;; APPLICATION NUMBER: US 09/016,464

;; FILING DATE: 30-January-1998

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Amzel, Viviana

;; REGISTRATION NUMBER: 30,930

;; REFERENCE/DOCKET NUMBER: EPI-00672

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: 609-409-3035

;; TELEFAX: 413-254-9245

;; TELEX: <Unknown>

;; INFORMATION FOR SEQ ID NO: 772:

;; SEQUENCE CHARACTERISTICS:

;; LENGTH: 11 base pairs

;; TYPE: nucleic acid

;; STRANDEDNESS: single

;; TOPOLOGY: linear

;; MOLECULE TYPE: DNA (genomic)

;; SEQUENCE DESCRIPTION: SEQ ID NO: 772:

US-09-093-972C-772

Query Match 52.5%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 58;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GCGGCGATCG 15

Db 1 GCGGCGATCG 10

RESULT 88

US-10-112-267-44/c
; Sequence 44, Application US/10112267
; Publication No. US20030068678A1
; GENERAL INFORMATION:
; APPLICANT: Botstein, David A.
; APPLICANT: Cohen, Robert
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Lawrence, David A.
; APPLICANT: Levine, Arnold J.
; APPLICANT: Pennica, Diane
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: WISP POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R2
; CURRENT APPLICATION NUMBER: US/10/112,267
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/182,145B
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/063,704
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-10-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/073,612
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-04
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/081,695
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-14
; NUMBER OF SEQ ID NOS: 156
; SEQ ID NO 44
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1-11_
; OTHER INFORMATION: Sequence is synthesized
US-10-112-267-44

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGG 10
||| |||||
Db 11 CGAGGGCGG 2

RESULT 89
US-10-214-417A-45
; Sequence 45, Application US/10214417A
; Publication No. US20030162190A1
; GENERAL INFORMATION:
; APPLICANT: GORENSTEIN, DAVID G.
; APPLICANT: LUXON, BRUCE A.
; APPLICANT: HERZOG, NORBERT
; APPLICANT: YANG, XIAN BIN
; TITLE OF INVENTION: PHOSPHOROMONOTHIOATE AND PHOSPHORODITHIOATE
; TITLE OF INVENTION: OLIGONUCLEOTIDE APTAMER CHIP FOR FUNCTIONAL PROTEOMICS
; FILE REFERENCE: UTMB:1011
; CURRENT APPLICATION NUMBER: US/10/214,417A
; CURRENT FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/334,887
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-214-417A-45

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGG 10
||| |||||
Db 1 CGGGGGCGG 10

RESULT 90
US-10-434-588-41/c
; Sequence 41, Application US/10434588
; Publication No. US20030171557A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; APPLICANT: Oku, Asuka
; TITLE OF INVENTION: NOVEL SERINE-THREONINE KINASE GENE
; FILE REFERENCE: 06501-033002
; CURRENT APPLICATION NUMBER: US/10/434,588
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: US/09/563,997
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: PCT/JP97/04855
; PRIOR FILING DATE: 1997-12-25
; PRIOR APPLICATION NUMBER: JP 8-357864
; PRIOR FILING DATE: 1996-12-27
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-434-588-41

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGG 10
||| |||||
Db 11 CGAGGGCGG 2

RESULT 91
US-10-628-770-24/c
; Sequence 24, Application US/10628770
; Publication No. US20040132052A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Diane
; APPLICANT: Pennica, Arnold J.
; TITLE OF INVENTION: POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: P1176R1
; CURRENT APPLICATION NUMBER: US/10/628,770
; CURRENT FILING DATE: 2003-07-28
; PRIOR APPLICATION NUMBER: US/09/182,562
; PRIOR FILING DATE: 1998-10-29
; NUMBER OF SEQ ID NOS: 52
; SEQ ID NO 24
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial sequence
; LOCATION: 1-11
; OTHER INFORMATION: Sequence is synthesized
US-10-628-770-24

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGCGG 10
Db 11 CGGAGGCGG 2

RESULT 92

US-10-762-154-32/c
; Sequence 32, Application US/10762154
; Publication No. US20040176574A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-Ichi
; TITLE OF INVENTION: TRANSPORTER GENES
; FILE REFERENCE: 06501-057001
; CURRENT APPLICATION NUMBER: US/10/762,154
; CURRENT FILING DATE: 2004-01-21
; PRIOR FILING DATE: 2000-03-07
; PRIOR APPLICATION NUMBER: JP 10/156660
; PRIOR FILING DATE: 1998-05-20
; PRIOR APPLICATION NUMBER: JP 9/260972
; PRIOR FILING DATE: 1997-09-08
; PRIOR APPLICATION NUMBER: PCT/JP98/04009
; PRIOR FILING DATE: 1998-09-07
; NUMBER OF SEQ ID NOS: 33
; SEQ ID NO 32
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Synthesized Adapte
US-10-762-154-32

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGCGG 10
Db 11 CGGAGGCGG 2

RESULT 93

US-10-659-549-23/c
; Sequence 23, Application US/10659549
; Publication No. US20040229307A1
; GENERAL INFORMATION:
; APPLICANT: Diane Pennica
; TITLE OF INVENTION: GUANYLATE-BINDING PROTEIN
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/659,549
; FILING DATE: 10-Sep-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/015,089A
; FILING DATE: 29-Jan-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Hasak, Janet E.
; REGISTRATION NUMBER: 28,616
; REFERENCE/DOCKET NUMBER: P1056

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1896
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 base pairs
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-659-549-23

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGCGG 10
Db 11 CGGAGGCGG 2

RESULT 94

US-10-758-451-677
; Sequence 677, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 677
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-677

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGGCGGC 11
Db 2 GCGAGGCGGC 11

RESULT 95

US-10-758-451-772
; Sequence 772, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 772
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-772

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 58;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
Db 1 GGCGGCATCG 10

RESULT 96
US-09-093-972C-654
; Sequence 654, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRUCTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 654:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 654:
US-09-093-972C-654

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGGC 11
Db 3 GGAGGGCGGC 12

RESULT 97

US-09-093-972C-771
; Sequence 771, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRUCTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 771:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 771:
US-09-093-972C-771

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
Db 1 GGCGGCATCG 10

RESULT 98
US-10-096-718-7/c
; Sequence 7, Application US/10096718
; Publication No. US20030032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; INTEGRATING
; TITLE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12

; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-7

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 GCGGCATCG 15
| | | | | | | |
Db 10 GTCGCATCG 1

RESULT 99

US-10-096-718-27
; Sequence 27, Application US/10096718
; Publication No. US2003032029A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/096,718
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC
US-10-096-718-27

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 GCGGCATCG 15
| | | | | | | |
Db 3 GTCGCATCG 12

RESULT 100

US-10-670-011-387
; Sequence 387, Application US/10670011
; Publication No. US20040209832A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Beigelman, Leonid
; APPLICANT: Pavco, Pamela
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: 400/132 (MBHB02-742-G)
; CURRENT APPLICATION NUMBER: US/10/670,011
; CURRENT FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782
; PRIOR FILING DATE: 2002-06-06

; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; PRIOR APPLICATION NUMBER: US60/409,293
; PRIOR FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: US60/440,129
; PRIOR FILING DATE: 2003-01-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 427
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense
US-10-670-011-387

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 2 GCGCGCGGC 11
| | | | | | | |
Db 1 GCGCGCGGC 10

RESULT 101

US-10-257-017B-277600
; Sequence 277600, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms (SNPs) and cytosin
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 277600
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0004520
US-10-257-017B-277600

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 2 GCGCGCGGC 11
| | | | | | | |
Db 3 GCGCGCGGC 12

RESULT 102

US-10-257-017B-314171
; Sequence 314171, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin

```
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; TITLE OF INVENTION: methylations
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 314171
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0026157
US-10-257-017B-314171

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGCG 10
   ||| |||||
Db 1 CGGAGGCGCG 10

RESULT 103
US-10-257-017B-322459/c
; Sequence 322459, Application US/10257017B
; Publication No. US20040241651A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Detection of single nucleotide polymorphisms [SNPs] and cytosine
; FILE REFERENCE: E01/1193/WO
; CURRENT APPLICATION NUMBER: US/10/257,017B
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 382046
; SEQ ID NO 322459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer for the detection of SNP TSC0030884
US-10-257-017B-322459

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGCG 10
   ||| ||||| ||
Db 11 CGCGGGGTGG 2

RESULT 104
US-10-758-451-654
; Sequence 654, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 654
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-654

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGCGGGCGCG 11
   || |||||
Db 3 GGAGGGCGCG 12

RESULT 105
US-10-758-451-771
; Sequence 771, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 771
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-771

Query Match          52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GGCGGCATCG 15
   ||||| ||
Db 1 GGCGGCATCG 10

RESULT 106
US-10-764-957-387
; Sequence 387, Application US/10764957
; Publication No. US20050054596A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: McSwiggen, James
; APPLICANT: Favco, Pamela
; APPLICANT: Beigelman, Leo
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor and Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/144 (MEHB02-742-O)
; CURRENT APPLICATION NUMBER: US/10/764,957
; CURRENT FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US60/358,580
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US60/363,124
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US60/386,782
```

; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US60/399,348
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: US60/406,784
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US60/408,378
; PRIOR FILING DATE: 2002-09-05
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 387
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: VEGF/VEGFR1 Homologous Target

US-10-764-957-387

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GGCGGGCGGC 11
| | | | |
Db 1 GGCGGGCGGC 10

RESULT 107

US-10-944-920-7/c
; Sequence 7, Application US/10944920
; Publication No. US20050136442A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; FILE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/944,920
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US/10/096,718
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 7
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC

US-10-944-920-7

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGGCATCG 15
| | | | |
Db 10 GTCGGCATCG 1

RESULT 108

US-10-944-920-27
; Sequence 27, Application US/10944920
; Publication No. US20050136442A1
; GENERAL INFORMATION:
; APPLICANT: Collins, Mark
; TITLE OF INVENTION: THREE DIMENSIONAL METHOD AND APPARATUS FOR
; TITLE OF INVENTION: INTEGRATING
; FILE OF INVENTION: SAMPLE PREPARATION AND MULTIPLEX ASSAYS
; FILE REFERENCE: 236/039
; CURRENT APPLICATION NUMBER: US/10/944,920

; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: US/10/096,718
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/217,472
; PRIOR FILING DATE: 1998-12-21
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Microsoft Word
; SEQ ID NO 27
; LENGTH: 12
; TYPE: DNA
; ORGANISM: SYNTHETIC

US-10-944-920-27

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGGCATCG 15
| | | | |
Db 3 GTCGGCATCG 12

RESULT 109

US-10-869-055B-3
; Sequence 3, Application US/10869055B
; Publication No. US20050214782A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Tao
; APPLICANT: Li, Jinghan
; APPLICANT: Chen, Te-Ming
; TITLE OF INVENTION: Generation and application of standardized universal libraries
; FILE REFERENCE: 85201-232
; CURRENT APPLICATION NUMBER: US/10/869,055B
; CURRENT FILING DATE: 2004-06-17
; PRIOR APPLICATION NUMBER: PCT/CA02/01941
; PRIOR FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: US 60/340009
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: forward pcr primer

US-10-869-055B-3

Query Match 52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GGCGGGCATCG 15
| | | | |
Db 3 GTCGGCATCG 12

RESULT 110

US-10-962-898-2263
; Sequence 2263, Application US/10962898
; Publication No. US20050222066A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Richards, Ivan
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/236 (MBHB02-742-U)
; CURRENT APPLICATION NUMBER: US/10/962,898
; CURRENT FILING DATE: 2004-10-12
; PRIOR APPLICATION NUMBER: US 10/944,644
; PRIOR FILING DATE: 2004-09-16

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; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2263
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-962-898-2263

Query Match      52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches      9; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 GCGCGGCGGC 11
Db      1 GCGCGGCGGC 10

RESULT 111
US-10-944-611-2263
; Sequence 2263, Application US/10944611
; Publication No. US2005023398A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Therapeutics, Inc.
; APPLICANT: Jadhav, Vasant
; APPLICANT: Kossen, Karl
; APPLICANT: Zinnen, Shawn
; APPLICANT: Vaish, Narendra
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition Of Vascular Endothelial
; TITLE OF INVENTION: Growth Factor And Vascular Endothelial Growth Factor Receptor
; TITLE OF INVENTION: Gene Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/235 (MEHB02-742-S)
; CURRENT APPLICATION NUMBER: US/10/944,611
; CURRENT FILING DATE: 2004-09-16
; PRIOR APPLICATION NUMBER: US 10/844,076
; PRIOR FILING DATE: 2004-05-11
; PRIOR APPLICATION NUMBER: US 10/831,620
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 10/764,957
; PRIOR FILING DATE: 2004-01-26
; PRIOR APPLICATION NUMBER: US 10/670,011
; PRIOR FILING DATE: 2003-09-23
; PRIOR APPLICATION NUMBER: US 10/665,255
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: US 10/664,767
; PRIOR FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: PCT/US03/05022
; PRIOR FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: US 60/393,796
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,348
; PRIOR FILING DATE: 2002-07-29
```

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; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4252
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2263
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA sense region
US-10-944-611-2263

Query Match      52.5%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 66;
Matches      9; Conservative      0; Mismatches      1; Indels      0; Gaps      0;

QY      2 GCGCGGCGGC 11
Db      1 GCGCGGCGGC 10

RESULT 112
US-09-154-750A-12/c
; Sequence 12, Application US/09154750A
; Publication No. US20020055097A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Polyak, Kornelia
; TITLE OF INVENTION: p53-Induced Apoptosis
; FILE REFERENCE: 1107.75357
; CURRENT APPLICATION NUMBER: US/09/154,750A
; CURRENT FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/059,153
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/079817
; PRIOR FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-154-750A-12

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches      8; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

QY      1 CGCGCGGC 8
Db      9 CGCGCGGC 2

RESULT 113
US-09-943-458-9/c
; Sequence 9, Application US/09943458
; Patent No. US20020110819A1
; GENERAL INFORMATION:
; APPLICANT: AVI Biopharma, Inc.
; TITLE OF INVENTION: Method for Analysis of Oligonucleotide
; TITLE OF INVENTION: Analogs
; FILE REFERENCE: 50450-8038.W000
; CURRENT APPLICATION NUMBER: US/09/943,458
; CURRENT FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/229,245
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
```

```

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fragment of complement to SEQ ID NO: 1
US-09-943-458-9

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 GGCATCGT 16
Db 10 GGCATCGT 3

RESULT 114
US-09-990-186-101
; Sequence 101, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-101

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGCGCG 10
Db 1 GCGGCGCG 8

RESULT 115
US-09-990-186-1277
; Sequence 1277, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1277

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GCGGCGCG 10
Db 1 GCGGCGCG 8

RESULT 116
US-09-990-186-1688
; Sequence 1688, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1688

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCGGCGCG 11
Db 1 CCGGCGCG 8

RESULT 117
US-09-990-186-1689
; Sequence 1689, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1689

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCGGCGCG 11
Db 1 CCGGCGCG 8

RESULT 118
US-09-989-994-101
; Sequence 101, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS

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; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-101

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCGG 10
Db 1 GCGGGCGG 8

RESULT 119
US-09-989-994-1277
; Sequence 1277, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1277

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GCGGGCGG 10
Db 1 GCGGGCGG 8

RESULT 120
US-09-989-994-1688
; Sequence 1688, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
```

```
; OTHER INFORMATION: DNA
US-09-989-994-1688

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
Db 1 CGGGCGGC 8

RESULT 121
US-09-989-994-1689
; Sequence 1689, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1689

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
Db 1 CGGGCGGC 8

RESULT 122
US-10-033-145-1242
; Sequence 1242, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1242
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1242

Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGCGG 9
Db 3 GCGGGCGG 10
```

```

RESULT 123
US-10-033-145-1653
; Sequence 1653, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033.145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1653
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1653

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 GGCATCGT 16
        |||||
DB      1 GGCATCGT 8

RESULT 124
US-10-247-857-16/c
; Sequence 16, Application US/10247857
; Publication No. US20030115642A1
; GENERAL INFORMATION:
; APPLICANT: Ruffy, Rebecca C.
; TITLE OF INVENTION: TOBACCO CULTIVAR NC 2000
; FILE REFERENCE: 5051-589
; CURRENT APPLICATION NUMBER: US/10/247,857
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/323,908
; PRIOR FILING DATE: 2001-09-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Coupling marker
US-10-247-857-16

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GGGCGGCA 12
        |||||
DB      10 GGGCGGCA 3

RESULT 125
US-10-330-627-628
; Sequence 628, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-630

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGGGGCG 9
        |||||
DB      3 GCGGGGCG 10

RESULT 126
US-10-330-627-629
; Sequence 629, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 629
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-629

Query Match      50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGGGGCG 9
        |||||
DB      3 GCGGGGCG 10

RESULT 127
US-10-330-627-630
; Sequence 630, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-630

```

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGCG 9
| | | | |
Db 3 GCGGGCG 10

RESULT 128

US-10-228-876-1/c
; Sequence 1, Application US/10228876
; Publication No. US20040038400A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Allan C.
; APPLICANT: Loros, Jennifer J.
; APPLICANT: Dunlap, Jay C.
; TITLE OF INVENTION: METHODS FOR REGULATING GENE EXPRESSION USING LIGHT
; FILE REFERENCE: DC-0194
; CURRENT APPLICATION NUMBER: US/10/228,876
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-228-876-1

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCGGCATC 14
| | | | |
Db 9 GCGGCATC 2

RESULT 129

US-10-301-875A-34/c
; Sequence 34, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; PRIOR FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-34

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCGGGCGC 11
| | | | |
Db 10 CCGGGCGC 3

RESULT 130

US-10-713-381-21/c
; Sequence 21, Application US/10713381
; Publication No. US20040221331A1
; GENERAL INFORMATION:
; APPLICANT: ALBERTSEN, MARC C.
; APPLICANT: FOX, TIMOTHY W.
; APPLICANT: GARNAAT, CARL W.
; APPLICANT: HUFFMAN, GARY
; APPLICANT: KENDALL, TIMMY L.
; TITLE OF INVENTION: MALE TISSUE-PREFERRED REGULATORY REGION AND METHOD OF
; FILE REFERENCE: USING SAME
; FILE REFERENCE: 578R
; CURRENT APPLICATION NUMBER: US/10/713,381
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 08/880,499
; PRIOR FILING DATE: 1997-06-23
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-713-381-21

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGGCGC 8
| | | | |
Db 10 CCGGGCGC 3

RESULT 131

US-10-666-923-32
; Sequence 32, Application US/10666923
; Publication No. US20040235002A1
; GENERAL INFORMATION:
; APPLICANT: HOLMES, Michael
; APPLICANT: TSE, Christin
; TITLE OF INVENTION: MULTIPLEX SCREENING ASSAYS
; FILE REFERENCE: 8325-0033 (S33-US1)
; CURRENT APPLICATION NUMBER: US/10/666,923
; CURRENT FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,345
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: ZFP 757 anxA8 binding site
US-10-666-923-32

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCGGGCGC 11
| | | | |
Db 1 CCGGGCGC 8

RESULT 132

US-09-974-974-10/c
; Sequence 10, Application US/09974974
; Publication No. US20030013095A1
; GENERAL INFORMATION:
; APPLICANT: Kazunari TAIRA
; APPLICANT: Masashi WARASHINA
; APPLICANT: Tomoko WARASHINA

; TITLE OF INVENTION: Nucleic acid enzymes acquiring an activity for cleaving a
; TITLE OF INVENTION: target RNA by recognizing another molecule

; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/09/974,974
; CURRENT FILING DATE: 2002-03-14
; PRIOR APPLICATION NUMBER: JP 2000-313320
; PRIOR FILING DATE: 2000-10-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn ver. 2.0

; SEQ ID NO 10
; LENGTH: 11
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: substrate
US-09-974-974-10

Query Match 48.8%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 79;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CGCGCGCGCGC 11
||| ||| |||
Db 11 CGCGCGACGCG 1

RESULT 133

US-09-841-963A-5
; Sequence 5, Application US/09841963A
; Patent No. US20020081601A1
; GENERAL INFORMATION:
; APPLICANT: Watson, Dennis K.
; APPLICANT: Papas, Takis S. (Deceased)
; APPLICANT: Papas, Tula C. (Legal Representative)
; TITLE OF INVENTION: Methods and compositions for the diagnosis and treatment of cancer
; TITLE OF INVENTION: based on transcription factor ETS2

; FILE REFERENCE: 10545-035-999
; CURRENT APPLICATION NUMBER: US/09/841,963A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US99/27805
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 06/109,850
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-841-963A-5

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GCGGCATCG 15
|||||
Db 2 GCGGCATCG 10

RESULT 134

US-09-371-900-18/c
; Sequence 18, Application US/09371900
; Patent No. US20020137700A1
; GENERAL INFORMATION:
; APPLICANT: FAUB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/371,900
FILING DATE: 11-Aug-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "synthetic oligonucleotide"

HYPOTHETICAL: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-371-900-18
Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 GCGCGCATC 14
|||||
Db 10 GCGTGCATC 2

RESULT 135

US-09-970-820-18/c
; Sequence 18, Application US/09970820
; Patent No. US20020170077A1
; GENERAL INFORMATION:
; APPLICANT: FAUB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/970,820
FILING DATE: 05-Oct-2001
CLASSIFICATION: <Unknown>

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-970-820-18

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGCGCATC 14
||| |||||
Db 10 GGCTGCATC 2

RESULT 136
US-09-986-718-18/c
; Sequence 18, Application US/09986718
; Publication No. US20020178458A1
; GENERAL INFORMATION:
; APPLICANT: FALB, DEAN A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/986,718
; FILING DATE: 09-No. US20020178458A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,573
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

;
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-986-718-18

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGCGCATC 14
||| |||||
Db 10 GGCTGCATC 2

RESULT 137
US-09-899-595-18/c
; Sequence 18, Application US/09899595
; Publication No. US20030018994A1
; GENERAL INFORMATION:
; APPLICANT: Aventis CropScience GmbH
; TITLE OF INVENTION: Promoters for gene expression in caryopses of plants
; FILE REFERENCE: 514413-3885
; CURRENT APPLICATION NUMBER: US/09/899,595
; CURRENT FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: DE 100 32 379.0
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-09-899-595-18

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGCGCGG 10
||| |||||
Db 10 GCGGCGCGG 2

RESULT 138
US-09-990-186-1284
; Sequence 1284, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1284

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCGATCG 15
||| |||||
Db 1 GCGGCGATCG 9
```

RESULT 139

US-09-093-972C-678
; Sequence 678, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 678:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 678:
US-09-093-972C-678

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGGGGCGG 10
||| |||||
Db 2 GGAGGGCGG 10

RESULT 140
US-09-093-972C-789
; Sequence 789, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 789:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 789:
US-09-093-972C-789

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCG 15
||| |||||
Db 1 GCGGCATCG 9

RESULT 141
US-09-989-994-1284
; Sequence 1284, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1284
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-989-994-1284

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CGGCGATCG 15
||| |||
DB 1 CGGCGCTCG 9

RESULT 142

US-10-033-145-205/c
; Sequence 205, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 205
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-205

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| |||||
DB 9 CGACGGGCG 1

RESULT 143

US-10-033-145-240
; Sequence 240, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 240
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-240

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| |||||
DB 2 CGACGGGCG 10

RESULT 144

US-10-033-145-476/c
; Sequence 476, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 476
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-476

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CGGCATCGT 16
||| |||||
DB 10 CGGCTCGT 2

RESULT 145

US-10-329-465-129
; Sequence 129, Application US/10329465
; Publication No. US20030165949A1
; GENERAL INFORMATION:
; APPLICANT: Wang et al.
; TITLE OF INVENTION: FUSION
; FILE REFERENCE: 27373/37928A
; CURRENT APPLICATION NUMBER: US/10/329,465
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: US 60/343,826
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 315
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-10-329-465-129

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCG 9
|| |||||
DB 2 CGACGGGCG 10

RESULT 146

US-10-223-765-210
; Sequence 210, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun

```

; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 210
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-210

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 5 GGGCGGCAT 13
Db 2 GGGCGGCAT 10

RESULT 147
US-10-330-627-27/c
; Sequence 27, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-27

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 5 GGGCGGCAT 13
Db 10 GGGCGGCAT 2

RESULT 148
US-10-330-627-57
; Sequence 57, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-57

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 4 CGGCGGCAC 12
Db 1 CAGGCGGCA 9

RESULT 149
US-10-330-627-129/c
; Sequence 129, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-129

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 7 GCGGCATCG 15
Db 9 GTGGCATCG 1

RESULT 150
US-10-330-627-239/c
; Sequence 239, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 239
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-239

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

```

QY 1 CGCGGGCGG 9
 Db 9 CGACGGGCG 1

RESULT 151

US-10-330-627-407/c
 ; Sequence 407, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 407
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-407

Query Match 46.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 6 GCGCGGCATC 14
 Db 9 GGCAGCATC 1

RESULT 152

US-10-330-627-1318/c
 ; Sequence 1318, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1318
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-1318

Query Match 46.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 GCGGGCGGC 11
 Db 10 GCCGGCGGC 2

RESULT 153

US-10-330-627-1346
 ; Sequence 1346, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.

; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1346
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-1346

Query Match 46.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 CGCGGGCGG 9
 Db 2 CGACGGGCG 10

RESULT 154

US-10-330-627-1464/c
 ; Sequence 1464, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1464
 ; LENGTH: 10
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-10-330-627-1464

Query Match 46.3%; Score 7.4; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 85;
 Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 GCGGGCGGC 11
 Db 10 GCCGGCGGC 2

RESULT 155

US-10-330-627-1530/c
 ; Sequence 1530, Application US/10330627
 ; Publication No. US20030175771A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Velculescu, Victor E.
 ; APPLICANT: Kinzler, Kenneth W
 ; APPLICANT: Vogelstein, Bert
 ; TITLE OF INVENTION: Human Transcriptomes
 ; FILE REFERENCE: 001107.00319
 ; CURRENT APPLICATION NUMBER: US/10/330,627
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 09/448,480
 ; PRIOR FILING DATE: 1999-11-24
 ; NUMBER OF SEQ ID NOS: 1564
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1530

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1530

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GCGGCGGC 11
Db 10 GCGGCGGC 2

RESULT 156
US-10-186-950-18/c
; Sequence 18, Application US/10186950
; Publication No. US20030188327A1
; GENERAL INFORMATION:
; APPLICANT: FALLB, DEAN A
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
; NUMBER OF SEQUENCES: 54
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/186,950
; FILING DATE: 02-Jul-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/944,496
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/599,654
; FILING DATE: 09-FEB-1996
; APPLICATION NUMBER: US 08/485,573
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/386,844
; FILING DATE: 10-FEB-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CORUZZI, LAURA A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "synthetic oligonucleotide"
; HYPOTHETICAL: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-186-950-18

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGCGGC 14
Db 9 GCGGCGGC 1
```

```
Db 10 GGCTGCATC 2

RESULT 157
US-10-314-578-1141/c
; Sequence 1141, Application US/10314578
; Publication No. US20030212026A1
; GENERAL INFORMATION:
; APPLICANT: Krieg, Arthur M.
; APPLICANT: Schetter, Christian
; APPLICANT: Vollmer, Jorg
; TITLE OF INVENTION: Immunostimulatory Nucleic Acids
; FILE REFERENCE: C1039/7035 (HCL/MAT)
; CURRENT APPLICATION NUMBER: US/10/314,578
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 60/156,113
; PRIOR FILING DATE: 1999-09-25
; PRIOR APPLICATION NUMBER: US 60/156,135
; PRIOR FILING DATE: 1999-09-27
; PRIOR APPLICATION NUMBER: US 60/227,436
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 1145
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1141
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
US-10-314-578-1141

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 GCGCATCGT 16
Db 9 CGACATCGT 1

RESULT 158
US-10-293-222-22/c
; Sequence 22, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-22

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GCGGCGATC 14
Db 9 GGCAGCATC 1
```

```
RESULT 159
US-10-293-222-24/c
; Sequence 24, Application US/10293222
; Publication No. US2004003392A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-24

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 3 GCGGCGCGC 11
Db 10 GCGGCGCGC 2

RESULT 160
US-10-228-876-2/c
; Sequence 2, Application US/10228876
; Publication No. US20040038400A1
; GENERAL INFORMATION:
; APPLICANT: Froehlich, Allan C.
; APPLICANT: Loros, Jennifer J.
; APPLICANT: Dunlap, Jay C.
; TITLE OF INVENTION: METHODS FOR REGULATING GENE EXPRESSION USING LIGHT
; FILE REFERENCE: DC-0194
; CURRENT APPLICATION NUMBER: US/10/228,876
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-228-876-2

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 7 GCGGCATCG 15
Db 9 GCGTCATCG 1

RESULT 161
US-10-301-875A-35/c
; Sequence 35, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
```

```
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-35

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 CCGCGGGCG 9
Db 10 CCGCGGGCG 2

RESULT 162
US-10-301-875A-36/c
; Sequence 36, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-301-875A-36

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches 8; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 4 CCGCGGGCA 12
Db 10 CCGCGGGCA 2

RESULT 163
US-10-758-451-678
; Sequence 678, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES,
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
```



```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 678
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-678

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCGCGGCGG 10
        ||| |||||
Db      2 GGAGGGCGG 10

RESULT 164
US-10-758-451-789
; Sequence 789, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF D
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; TITLE OF INVENTION: INFLAMMATION
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 789
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-789

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 GCGGCATCG 15
        ||| |||||
Db      1 GCGGCATCG 9

RESULT 165
US-10-805-292-164
; Sequence 164, Application US/10805292
; Publication No. US20050026176A1
; GENERAL INFORMATION:
; APPLICANT: Yoshii, Hiroto
; APPLICANT: Fukui, Toshifumi
; TITLE OF INVENTION: DNA PROBE DESIGNING APPARATUS AND INFORMATION PROCESSING METHOD
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 03560.003438
; CURRENT APPLICATION NUMBER: US/10/805,292
; CURRENT FILING DATE: 2004-03-22
; PRIOR APPLICATION NUMBER: JPA2003-099464
; PRIOR FILING DATE: 2003-04-02
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 164
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: DNA exemplified in the drawing
US-10-805-292-164

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;

US-10-805-292-164

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 678
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-678

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CGCGGGCGG 9
        ||| |||||
Db      2 CGCGGGGACG 10

RESULT 166
US-10-827-659-217/c
; Sequence 217, Application US/10827659
; Publication No. US20050235382A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: Docket number 38-21 (52710)C
; CURRENT APPLICATION NUMBER: US/10/827,659
; CURRENT FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-827-659-217

Query Match      46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 85;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GCGGGGCGG 10
        ||| |||||
Db      10 GCGGGGCGG 2

RESULT 167
US-10-091-281-459
; Sequence 459, Application US/10091281
; Publication No. US20030190617A1
; GENERAL INFORMATION:
; APPLICANT: RAYMOND, VINCENT
; APPLICANT: SI, ERWIN
; APPLICANT: MORISSETTE, JEAN
; TITLE OF INVENTION: OPTINEURIN NUCLEIC ACID MOLECULES AND USES THEREOF
; FILE REFERENCE: 13587.338
; CURRENT APPLICATION NUMBER: US/10/091,281
; CURRENT FILING DATE: 2002-03-06
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 459
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Putative AP2F/AP2.01 motif
US-10-091-281-459

Query Match      45.0%; Score 7.2; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 1.2e+02;
Matches      9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 CGCGCGGCGGCA 12
        ||| |||||
Db      1 CGCGCGGCGGCA 12

RESULT 168
US-09-758-073-5/c
; Sequence 5, Application US/09758073
; Patent No. US20010024785A1
; GENERAL INFORMATION:
; APPLICANT: Keinath, et al.
; TITLE OF INVENTION: Method of Diagnosing Gummy Stem Blight in
; TITLE OF INVENTION: Plants Using a Polymerase Chain Reaction Assay
```

```
;/ NUMBER OF SEQUENCES: 16
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Judy C. Jarecki-Black, Ph.D.
;/ ADDRESSEE: Dority & Manning, P.A.
;/ STREET: 700 E. No. US20010024785A1th Street, Suite 15
;/ CITY: Greenville
;/ STATE: South Carolina
;/ COUNTRY: USA
;/ ZIP: 29601
;/
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
;/
;/ COMPUTER: IBM compatible
;/ OPERATING SYSTEM: MS Dos; Windows 95
;/ SOFTWARE: WordPerfect 6.1
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/758,073
;/ FILING DATE: Filed Herewith
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 60/078,103
;/ FILING DATE: 16-MAR-1998
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Judy C. Jarecki-Black, Ph.D.
;/ REGISTRATION NUMBER: P44,170
;/ REFERENCE/DOCKET NUMBER: CXU-291
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (864) 271-1592
;/ TELEFAX: (864) 233-7342
;/ INFORMATION FOR SEQ ID NO: 5:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 Pairs
;/ TYPE: Nucleic Acid
;/ STRANDEDNESS: Single
;/ TOPOLOGY: Linear
;/ MOLECULE TYPE: Other Nucleic Acid
;/ DESCRIPTION: Oligonucleotide Primer
;/ HYPOTHETICAL: No
;/ ANTI-SENSE: No
;/ ORIGINAL SOURCE: Operon Technologies (Alameda, CA)
;/ IMMEDIATE SOURCE: Operon Technologies
;/ POSITION IN GENOME: No. US20010024785A1 Applicable
;/ UNITS:
;/ FEATURE:
;/ OTHER INFORMATION: Commercially Available Primer
;/ PUBLICATION INFORMATION: No. US20010024785A1 Applicable
;/
;/ US-09-758-073-5
;/
;/ Query Match 43.8%; Score 7; DB 1; Length 10;
;/ Best Local Similarity 100.0%; Pred. No. 1e+02;
;/ Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;/
;/ QY 7 GCGGCAT 13
;/ Db 8 GCGGCAT 2
;/
;/ RESULT 169
;/ US-09-811-259-4
;/ Sequence 4, Application US/09811259
;/ Patent No. US20020052483A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Daniel K. Podolsky
;/ TITLE OF INVENTION: INTESTINAL TREFOIL PROTEINS
;/ NUMBER OF SEQUENCES: 20
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Fish & Richardson, P.C.
;/ STREET: 225 Franklin Street
;/ CITY: Boston
;/ STATE: MA
;/ COUNTRY: US
;/ ZIP: 02110-2804
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Diskette
```

```
;/ COMPUTER: IBM Compatible
;/ OPERATING SYSTEM: Windows95
;/ SOFTWARE: FastSeq for Windows Version 2.0
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/811,259
;/ FILING DATE: 16-Mar-2001
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 08/631,469
;/ FILING DATE: 12-APR-1996
;/ APPLICATION NUMBER: 08/191,352
;/ FILING DATE: 02-FEB-1994
;/ APPLICATION NUMBER: 08/037,741
;/ FILING DATE: 25-MAR-1993
;/ APPLICATION NUMBER: 07/837,192
;/ FILING DATE: 13-FEB-1992
;/ APPLICATION NUMBER: 07/655,965
;/ FILING DATE: 14-FEB-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Melkicjohn, Ph.D., Anita L.
;/ REGISTRATION NUMBER: 35,283
;/ REFERENCE/DOCKET NUMBER: 00786/322001
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 617-542-5070
;/ TELEFAX: 617-542-8906
;/ TELEX: 200107
;/ INFORMATION FOR SEQ ID NO: 4:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 10 base pairs
;/ TYPE: nucleic acid
;/ STRANDEDNESS: single
;/ TOPOLOGY: linear
;/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
;/
;/ US-09-811-259-4
;/
;/ Query Match 43.8%; Score 7; DB 1; Length 10;
;/ Best Local Similarity 100.0%; Pred. No. 1e+02;
;/ Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;/
;/ QY 5 GGGCGGC 11
;/ Db 1 GGGCGGC 7
;/
;/ RESULT 170
;/ US-09-789-996-45
;/ Sequence 45, Application US/09789996
;/ Publication No. US20030013119A1
;/ GENERAL INFORMATION:
;/ APPLICANT: Margolskee, Robert F.
;/ TITLE OF INVENTION: Gustducin Materials and Methods
;/ NUMBER OF SEQUENCES: 46
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: MARSHALL, GERSTEIN & BORUN
;/ STREET: 6300 Sears Tower, 233 S. Wacker Drive
;/ CITY: Chicago
;/ STATE: Illinois
;/ COUNTRY: USA
;/ ZIP: 60606-6402
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/09/789,996
;/ FILING DATE: 21-Feb-2001
;/ CLASSIFICATION: <Unknown>
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 09/421,796
;/ FILING DATE: 10-OCT-1999
;/ APPLICATION NUMBER: US 08/124,807
;/ FILING DATE: 28-JUL-1998
;/ APPLICATION NUMBER: US 08/407,804
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; FILING DATE: 20-MAR-1995
; APPLICATION NUMBER: US 08/045,801
; FILING DATE: 08-APR-1993
; APPLICATION NUMBER: US 07/868,353
; FILING DATE: 09-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. US20030013119Aland, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 28038/37158
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-789-996-45

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 1 GGGCGGC 7

RESULT 171
US-09-990-186-1640
; Sequence 1640, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1640

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGCGCA 12
Db 3 GGGCGCA 9

RESULT 172
US-09-990-186-1641
; Sequence 1641, Application US/09990186
; Publication No. US20030068675A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.21 / S11-US3
; CURRENT APPLICATION NUMBER: US/09/990,186
; CURRENT FILING DATE: 2001-11-20
```

```
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-09-990-186-1641

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGGCGCA 12
Db 3 GGGCGCA 9

RESULT 173
US-09-093-972C-843
; Sequence 843, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCONSTRICTION, ALLERGY (IES) & INFLAMMATION
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 843:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 843:
US-09-093-972C-843
```

```
Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGGGGC 8
      |||||
Db      4 GCGGGGC 10

RESULT 174
US-09-093-972C-854
; Sequence 854, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 854:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 854:
US-09-093-972C-854

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 GCGGGGC 8
      |||||
Db      2 GCGGGGC 8

RESULT 176
US-09-093-972C-873
; Sequence 873, Application US/09093972C
; Publication No. US20030087845A1
; GENERAL INFORMATION:
; APPLICANT: Nyce, Jonathan W.
; TITLE OF INVENTION: COMPOSITION, FORMULATIONS & METHOD FOR PREVENTION
; & TREATMENT OF DISEASES & CONDITIONS ASSOCIATED WITH
; BRONCHOCOCONSTRICTION, ALLERGY(IES) & INFLAMMATION
;
; NUMBER OF SEQUENCES: 996
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EPIGENESIS PHARMACEUTICALS, INC.
; STREET: 7 Clarke Drive
```

```

; CITY: Cranbury
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 08512
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/093,972C
; FILING DATE: 09-Jun-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 08/757,024
; FILING DATE: 26-11-1996
; APPLICATION NUMBER: US 08/472,527
; FILING DATE: 7-June-1995
; APPLICATION NUMBER: US 09/016,464
; FILING DATE: 30-January-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Amzel, Viviana
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: EPI-00672
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 609-409-3035
; TELEFAX: 413-254-9245
; TELEX: <Unknown>
;
; INFORMATION FOR SEQ ID NO: 873:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 873:
US-09-993-972C-873

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCGGGC 8
| | | | |
Db 1 GCGGGC 7

RESULT 177
US-09-953-562-27
; Sequence 27, Application US/09953562
; Publication No. US20030096241A1
; GENERAL INFORMATION:
; APPLICANT: ZERIA PHARMACEUTICALS CO., LTD.
; TITLE OF INVENTION: METHOD OF SCREENING A DRUG FOR TREATMENT OF SQUAMOUS
; FILE REFERENCE: B6114-01
; CURRENT APPLICATION NUMBER: US/09/953,562
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: JP 2001-083352
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: homo sapiens
US-09-953-562-27

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 8 CGGCATC 14
| | | | |
Db 3 CGGCATC 9

```

```

RESULT 178
US-09-989-994-1640
; Sequence 1640, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1640

```

```

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 GCGGGCA 12
| | | | |
Db 3 GCGGGCA 9

```

```

RESULT 179
US-09-989-994-1641
; Sequence 1641, Application US/09989994
; Publication No. US20030104526A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/09/989,994
; CURRENT FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-09-989-994-1641

```

```

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 6 GCGGGCA 12
| | | | |
Db 3 GCGGGCA 9

```

```

RESULT 180
US-10-033-145-11/c
; Sequence 11, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION

```

```
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-11

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 CGGCGGG 7
        |||||
Db       8 CGGCGGG 2

RESULT 181
US-10-033-145-441/c
; Sequence 441, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 441
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-441

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      7 GCGGCAT 13
        |||||
Db       8 GCGGCAT 2

RESULT 182
US-10-033-145-855/c
; Sequence 855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 855

; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-11

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      1 CGGCGGG 7
        |||||
Db       8 CGGCGGG 2

RESULT 181
US-10-033-145-441/c
; Sequence 441, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 441
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-441

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      7 GCGGCAT 13
        |||||
Db       8 GCGGCAT 2

RESULT 182
US-10-033-145-855/c
; Sequence 855, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 855

; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-11

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      5 GCGCGGC 11
        |||||
Db      10 GCGCGGC 4

RESULT 183
US-10-033-145-1468
; Sequence 1468, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1468
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1468

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      3 GCGGGCG 9
        |||||
Db       3 GCGGGCG 9

RESULT 184
US-10-033-145-1516/c
; Sequence 1516, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1516
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-1516

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; 0; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0;

QY      6 GCGGCGA 12
        |||||
```

```

Db      8 GCGCGCA 2

RESULT 185
US-10-033-145-2124/c
; Sequence 2124, Application US/10033145
; Publication No. US2002015151A1
; GENERAL INFORMATION:
; APPLICANT: GENZYME CORPORATION
; APPLICANT: ROBERTS, BRUCE
; APPLICANT: SHANKARA, SRINIVAS
; TITLE OF INVENTION: PREPARATION AND USE OF SUPERIOR VACCINES
; FILE REFERENCE: GA0201C
; CURRENT APPLICATION NUMBER: US/10/033,145
; CURRENT FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: PCT/US99/13800
; PRIOR FILING DATE: 1999-06-18
; NUMBER OF SEQ ID NOS: 2137
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2124
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-033-145-2124

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCGGG 7
        |||||
Db      8 CCGCGGG 2

RESULT 186
US-10-141-263-5
; Sequence 5, Application US/10141263
; Publication No. US20020165196A1
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; TITLE OF INVENTION: Oligonucleotide Inhibitors of Cancer
; TITLE OF INVENTION: Cell Proliferation
; FILE REFERENCE: WIC01-NP003
; CURRENT APPLICATION NUMBER: US/10/141,263
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,166
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-141-263-5

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCGGG 7
        |||||
Db      2 CCGCGGG 8

RESULT 187
US-10-141-263-6/c
; Sequence 6, Application US/10141263
; Publication No. US20020165196A1
; GENERAL INFORMATION:
; APPLICANT: Wickstrom, Eric
; TITLE OF INVENTION: Oligonucleotide Inhibitors of Cancer
; TITLE OF INVENTION: Cell Proliferation
; FILE REFERENCE: WIC01-NP003
; CURRENT APPLICATION NUMBER: US/10/141,263
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,166
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-141-263-6

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCGCGGG 7
        |||||
Db      2 CCGCGGG 8

RESULT 188
US-10-313-642-5
; Sequence 5, Application US/10313642
; Publication No. US20030134797A1
; GENERAL INFORMATION:
; APPLICANT: Podolsky, Daniel K.
; TITLE OF INVENTION: Intestinal Trefoil Proteins
; FILE REFERENCE: 50206/432002
; CURRENT APPLICATION NUMBER: US/10/313,642
; CURRENT FILING DATE: 2002-12-06
; PRIOR APPLICATION NUMBER: US 09/313,434
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide for PCR
US-10-313-642-5

Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 GCGCGGC 11
        |||||
Db      1 GCGCGGC 7

RESULT 189
US-10-223-765-201
; Sequence 201, Application US/10223765
; Publication No. US20030165997A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jin-Soo
; APPLICANT: Bae, Kwang-Hee
; APPLICANT: Park, Kyung-Soon
; APPLICANT: Kwon, Young Do
; APPLICANT: Ryu, Eun-Hyun
; APPLICANT: Hwang, Moon-Sun
; TITLE OF INVENTION: ZINC FINGER DOMAIN LIBRARIES
; FILE REFERENCE: 12279-005001
; CURRENT APPLICATION NUMBER: US/10/223,765
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: 60/374,355
; PRIOR FILING DATE: 2002-04-22

```

```
; PRIOR APPLICATION NUMBER: 60/313,402
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated oligonucleotide
US-10-223-765-201

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGG 7
Db 2 CGCGGGG 8

RESULT 190
US-10-330-627-367/c
; Sequence 367, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 367
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-367

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 10 CGGCATC 4

RESULT 191
US-10-330-627-384/c
; Sequence 384, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 384
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-384

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 10 CGGCATC 4

RESULT 192
US-10-330-627-923
; Sequence 923, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-923

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 7 GCGGGGC 1

RESULT 193
US-10-330-627-924
; Sequence 924, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 924
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-924

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 3 GCGGGGC 9

RESULT 194
US-10-330-627-924
; Sequence 924, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 924
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-924

Query Match          43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGGGGC 8
Db 3 GCGGGGC 9

RESULT 194
US-10-330-627-924
```


US-10-330-627-938/c
; Sequence 938, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: Human Transcriptsomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 938
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-938

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 9 GGGCGGC 3

RESULT 195
US-10-330-627-1120/c
; Sequence 1120, Application US/10330627
; Publication No. US20030175771A1
; GENERAL INFORMATION:
; APPLICANT: Velculescu, Victor E.
; APPLICANT: Kinzler, Kenneth W.
; TITLE OF INVENTION: Human Transcriptsomes
; FILE REFERENCE: 001107.00319
; CURRENT APPLICATION NUMBER: US/10/330,627
; CURRENT FILING DATE: 2002-12-30
; PRIOR APPLICATION NUMBER: US 09/448,480
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 1564
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1120
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-330-627-1120

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 7 GGGCGGC 1

RESULT 196
US-10-356-792-21
; Sequence 21, Application US/10356792
; Publication No. US20030215842A1
; GENERAL INFORMATION:
; APPLICANT: Sledziewski, Andrzej
; APPLICANT: Schweikhardt, Gary
; TITLE OF INVENTION: METHOD FOR THE ANALYSIS OF CYTOSINE METHYLATION PATTERNS
; FILE REFERENCE: 47675-33
; CURRENT APPLICATION NUMBER: US/10/356,792
; CURRENT FILING DATE: 2003-01-30
; PRIOR APPLICATION NUMBER: 60/352,944

; PRIOR FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: AP-PCR Primer CG5
US-10-356-792-21

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 4 GGGCGGC 10

RESULT 197
US-10-259-723-2
; Sequence 2, Application US/10259723
; Publication No. US20030219764A1
; GENERAL INFORMATION:
; APPLICANT: Gene Networks, Inc.
; APPLICANT: Imoto, Seiya
; APPLICANT: Goto, Takao
; APPLICANT: Miyano, Satoru
; APPLICANT: Toshiro, Kosuke
; APPLICANT: Hoon, Michiel de
; APPLICANT: Savoie, Christopher J.
; APPLICANT: Kuhara, Satoru
; TITLE OF INVENTION: BIOLOGICAL DISCOVERY USING GENE REGULATORY NETWORKS GENERATED FROM
; FILE REFERENCE: GENN1000US1
; CURRENT APPLICATION NUMBER: US/10/259,723
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/325,016
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: 60/334,230
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/370,824
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: 60/334,372
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/334,255
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 60/397,458
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-259-723-2

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
| | | | |
Db 2 GGGCGGC 8

RESULT 198
US-10-353-334-4
; Sequence 4, Application US/10353334
; Publication No. US20030225250A1
; GENERAL INFORMATION:
; APPLICANT: Daniel K. Podoleky

```
; TITLE OF INVENTION: INTERSTINAL TREFOIL PROTEINS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEES: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/353,334
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/631,469B
; FILING DATE: 12-Apr-1996
; APPLICATION NUMBER: 08/631,469
; FILING DATE: 12-APR-1996
; APPLICATION NUMBER: 08/191,352
; FILING DATE: 02-FEB-1994
; APPLICATION NUMBER: 08/037,741
; FILING DATE: 25-MAR-1993
; APPLICATION NUMBER: 07/837,192
; FILING DATE: 13-FEB-1992
; APPLICATION NUMBER: 07/655,965
; FILING DATE: 14-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 00786/322001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-542-5070
; TELEFAX: 617-542-8906
; TELEX: 200107
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-353-334-4

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db 1 GGGCGGC 7

RESULT 199
US-10-293-222-190/c
; Sequence 190, Application US/10293222
; Publication No. US20040033932A1
; GENERAL INFORMATION:
; APPLICANT: Versteeg, Rogier
; APPLICANT: Caron, Hubertus N.
; TITLE OF INVENTION: MYC targets
; FILE REFERENCE: 2183-5580US
; CURRENT APPLICATION NUMBER: US/10/293,222
; CURRENT FILING DATE: 2002-11-12
; PRIOR APPLICATION NUMBER: PCT/NL01/00361
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: EP 00201698.8
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: EP 00202284.6
; PRIOR FILING DATE: 2000-06-29
```

```
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 190
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-293-222-190

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CGGCATC 14
Db 10 CGGCATC 4

RESULT 200
US-10-301-875A-9/c
; Sequence 9, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-9

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. le+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGGCGGC 11
Db 9 GGGCGGC 3

RESULT 201
US-10-301-875A-20/c
; Sequence 20, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301,875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-20
```

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 202

US-10-301-875A-33/c
; Sequence 33, Application US/10301875A
; Publication No. US20040091874A1
; GENERAL INFORMATION:
; APPLICANT: YAMASAKI, KAZUHIKO
; APPLICANT: HAO, DONGYUN
; TITLE OF INVENTION: SENSOR CHIP FOR NUCLEIC ACID SELECTION
; FILE REFERENCE: 081356/0179
; CURRENT APPLICATION NUMBER: US/10/301.875A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: JP 2002/149330
; PRIOR FILING DATE: 2002-05-23
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-301-875A-33

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGG 7
| | | | |
Db 8 CGGCGGG 2

RESULT 203

US-10-794-929-32/c
; Sequence 32, Application US/10794929
; Publication No. US20040166526A1
; GENERAL INFORMATION:
; APPLICANT: OMNISCIENCE PHARMACEUTICALS
; APPLICANT: Chaparian, Michael
; APPLICANT: Zheng, Shu-Xian
; TITLE OF INVENTION: GENE CLONING
; FILE REFERENCE: 1002.00011
; CURRENT APPLICATION NUMBER: US/10/794,929
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 10/049,994
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/22743
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,788
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/149,822
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: decamer OS-DEC-004

US-10-794-929-32

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 204

US-10-794-929-33/c
; Sequence 33, Application US/10794929
; Publication No. US20040166526A1
; GENERAL INFORMATION:
; APPLICANT: OMNISCIENCE PHARMACEUTICALS
; APPLICANT: Chaparian, Michael
; APPLICANT: Zheng, Shu-Xian
; TITLE OF INVENTION: GENE CLONING
; FILE REFERENCE: 1002.00011
; CURRENT APPLICATION NUMBER: US/10/794,929
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: 10/049,994
; PRIOR FILING DATE: 2002-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/22743
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,788
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: 60/149,822
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 33
; LENGTH: 10
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
; OTHER INFORMATION: decamer OS-DEC-005
US-10-794-929-33

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
| | | | |
Db 10 GGGCGGC 4

RESULT 205

US-10-602-494-360
; Sequence 360, Application US/10602494
; Publication No. US20040265833A1
; GENERAL INFORMATION:
; APPLICANT: Cathy Lofton-Day
; APPLICANT: Andrew Sledziewski
; APPLICANT: Jeff Thomas
; APPLICANT: Robert W. Day
; APPLICANT: Lori Tonnes-Priddy
; APPLICANT: Karen Cardon
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of colorectal cell
; FILE REFERENCE: 47675-45
; CURRENT APPLICATION NUMBER: US/10/602,494
; CURRENT FILING DATE: 2003-06-23
; NUMBER OF SEQ ID NOS: 385
; SEQ ID NO 360
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens

US-10-602-494-360

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GGCGGC 11
|||||
Db 4 GGCGGC 10

RESULT 206
US-10-758-451-843
; Sequence 843, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 843
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-843

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGC 8
|||||
Db 4 GGCGGC 10

RESULT 207
US-10-758-451-854
; Sequence 854, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 854
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-854

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGC 8
|||||
Db 3 GGCGGC 9

RESULT 208

US-10-758-451-864
; Sequence 864, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 864
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-864

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGC 8
|||||
Db 2 GGCGGC 8

RESULT 209

US-10-758-451-873
; Sequence 873, Application US/10758451
; Publication No. US20050014711A1
; GENERAL INFORMATION:
; APPLICANT: East Carolina University
; TITLE OF INVENTION: COMPOSITION, FORMULATION & METHOD FOR PREVENTION & TREATMENT OF
; TITLE OF INVENTION: AND CONDITIONS ASSOCIATED WITH BRONCHOCONSTRICTION, ALLERGY (IES)
; FILE REFERENCE: 30775-706.301
; CURRENT APPLICATION NUMBER: US/10/758,451
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 09/093,972
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 996
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 873
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-758-451-873

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGCGGC 8
|||||
Db 1 GGCGGC 7

RESULT 210

US-10-497-764-27
; Sequence 27, Application US/10497764
; Publication No. US20050124598A1
; GENERAL INFORMATION:
; APPLICANT: Invenux, Inc.
; APPLICANT: Tarasow, Ted
; APPLICANT: Dewey, Torin
; APPLICANT: Eaton, Bruce
; APPLICANT: Nieuwlandt, Dan
; TITLE OF INVENTION: Antibiotic Compounds

```
; FILE REFERENCE: INX 2636-119PCT
; CURRENT APPLICATION NUMBER: US/10/497,764
; CURRENT FILING DATE: 2004-06-04
; PRIOR APPLICATION NUMBER: 60/340,255
; PRIOR FILING DATE: 2001-12-18
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Sequence
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: 5' nucleotide is conjugated to diene reactant 13 or 14 via 2000MW
; OTHER INFORMATION: PEG linker
US-10-497-764-27
```

```
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGGG 7
Db 4 CGGCGGG 10
|||||
```

```
RESULT 211
US-10-827-659-225/c
; Sequence 225, Application US/10827659
; Publication No. US20050235382A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology LLC
; TITLE OF INVENTION: PLANT REGULATORY SEQUENCES FOR SELECTIVE CONTROL
; FILE REFERENCE: Docket number 38-21 (S2710)C
; CURRENT APPLICATION NUMBER: US/10/827,659
; CURRENT FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 225
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Zea mays
US-10-827-659-225
```

```
Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GGGCGGC 11
Db 10 GGGCGGC 4
|||||
```

```
Search completed: May 9, 2006, 16:47:25
Job time : 1 secs
```


GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:49:14 ; Search time 0.001 Seconds
(without alignments)
6.912 Million cell updates/sec

Title: US-09-904-968A-20-COPY
Perfect score: 16
Sequence: 1 cggcggcgcatcgt 16

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 0.5

Searched: 21 seqs, 216 residues

Total number of hits satisfying chosen parameters: 42

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 21 summaries

Database : pubnewdb20.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	8.4	52.5	11	US-10-512-214-4	Sequence 4, Appli
C 2	8.4	52.5	11	US-10-766-560-9	Sequence 9, Appli
C 3	8.4	52.5	11	US-11-182-592-10	Sequence 10, Appl
C 4	8.4	50.0	10	US-11-225-686-101	Sequence 101, App
C 5	8.4	50.0	10	US-11-225-686-1277	Sequence 1277, Ap
C 6	8.4	50.0	10	US-11-225-686-1688	Sequence 1688, Ap
C 7	8.4	50.0	10	US-11-225-686-1689	Sequence 1689, Ap
C 8	8.4	50.0	10	US-11-202-009-101	Sequence 101, App
C 9	8.4	50.0	10	US-11-202-009-1277	Sequence 1277, Ap
C 10	8.4	50.0	10	US-11-202-009-1688	Sequence 1688, Ap
C 11	8.4	50.0	10	US-11-202-009-1689	Sequence 1689, Ap
C 12	7.8	48.8	11	US-10-523-055-8	Sequence 8, Appli
C 13	7.8	48.8	11	US-11-158-209-104	Sequence 104, App
C 14	7.8	48.8	11	US-11-158-209-1201	Sequence 1201, App
C 15	7.4	46.3	10	US-11-225-686-1284	Sequence 1284, Ap
C 16	7.4	46.3	10	US-11-202-009-1284	Sequence 1284, Ap
C 17	7.4	43.8	10	US-10-962-756A-46	Sequence 46, Appl
C 18	7.4	43.8	10	US-11-225-686-1640	Sequence 1640, Ap
C 19	7.4	43.8	10	US-11-225-686-1641	Sequence 1641, Ap
C 20	7.4	43.8	10	US-11-202-009-1640	Sequence 1640, Ap
C 21	7.4	43.8	10	US-11-202-009-1641	Sequence 1641, Ap

ALIGNMENTS

RESULT 1

US-10-512-214-4/c
; Sequence 4, Application US/10512214
; Publication No. US20050255103A1
; GENERAL INFORMATION:
; APPLICANT: NEZU, Jun-ichi
; TITLE OF INVENTION: Therapeutic Reagent for Lung Carcinoma

FILE REFERENCE: 382.1046
; CURRENT APPLICATION NUMBER: US/10/512,214
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: JP 2002-124743
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-512-214-4

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGCGGCGCG 10
Db 11 CCGAGGCGCG 2

RESULT 2

US-10-766-560-9/c
; Sequence 9, Application US/10766560
; Publication No. US20050281837A1
; GENERAL INFORMATION:
; APPLICANT: Pizza, Mariagrazia
; APPLICANT: Bartoloni, Antonella
; TITLE OF INVENTION: IMMUNOLOGICALLY ACTIVE POLYPEPTIDES WITH ALTERED TOXICITY USEFUL
; TITLE OF INVENTION: PREPARATION OF AN ANTIPERTUSSIS VACCINE
; FILE REFERENCE: 002441.00076
; CURRENT APPLICATION NUMBER: US/10/766,560
; CURRENT FILING DATE: 2004-01-29
; PRIOR APPLICATION NUMBER: US 08/261,668
; PRIOR FILING DATE: 1994-06-17
; PRIOR APPLICATION NUMBER: US 08/012,243
; PRIOR FILING DATE: 1993-02-01
; PRIOR APPLICATION NUMBER: US 07/265,742
; PRIOR FILING DATE: 1988-11-01
; PRIOR APPLICATION NUMBER: ITALY 22481 A/87
; PRIOR FILING DATE: 1987-11-02
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 9
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Bordetella pertussis
US-10-766-560-9

Query Match 52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCTTCGT 16
Db 11 GCGGCTTCGT 2

RESULT 3

US-11-182-592-10/c
; Sequence 10, Application US/11182592
; Publication No. US20050250153A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; APPLICANT: Ose, Asuka
; TITLE OF INVENTION: NOVEL FETAL GENES
; FILE REFERENCE: 14875-089001 (previously 06501-089001)
; CURRENT APPLICATION NUMBER: US/11/182,592
; CURRENT FILING DATE: 2005-07-14
; PRIOR APPLICATION NUMBER: US/09/974,143

```
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: PCT/JP00/02281
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 11/103356
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificially synthesized adapter sequence
US-11-182-592-10
```

```
Query Match          52.5%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 3.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 CGCGGGCGG 10
        ||| |||||
Db       11 CGGAGGGCG 2
```

```
RESULT 4
US-11-225-686-101
; Sequence 101, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-101
```

```
Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 CGCGGGCGG 10
        ||| |||||
Db       1 CGCGGGCGG 8
```

```
RESULT 5
US-11-225-686-1277
; Sequence 1277, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
```

```
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1277
```

```
Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 CGCGGGCGG 10
        ||| |||||
Db       1 CGCGGGCGG 8
```

```
RESULT 6
US-11-225-686-1688
; Sequence 1688, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1688
```

```
Query Match          50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      4 CGGGGCGGC 11
        ||| |||||
Db       1 CGGGGCGGC 8
```

```
RESULT 7
US-11-225-686-1689
; Sequence 1689, Application US/11225686
; Publication No. US20060019349A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/225,686
; CURRENT FILING DATE: 2005-09-12
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1689
```


Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
DB 1 CGGGCGGC 8

RESULT 8
US-11-202-009-101
; Sequence 101, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-101

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGGCGGC 10
| | | | |
DB 1 CGGGCGGC 8

RESULT 9
US-11-202-009-1277
; Sequence 1277, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1277
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-1277

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGGGCGGC 10
| | | | |

DB 1 CGGGCGGC 8

RESULT 10
US-11-202-009-1688
; Sequence 1688, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1688
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-1688

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
DB 1 CGGGCGGC 8

RESULT 11
US-11-202-009-1689
; Sequence 1689, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1689
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-1689

Query Match 50.0%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGGCGGC 11
| | | | |
DB 1 CGGGCGGC 8

RESULT 12
US-10-523-055-8/c
; Sequence 8, Application US/10523055
; Publication No. US20060057160A1

OTHER INFORMATION: DNA
US-11-225-686-1284

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCG 15
| | | | | | | |
DB 1 GCGGCGTCG 9

RESULT 16

US-11-202-009-1284
Sequence 1284, Application US/11202009
Publication No. US20060024726A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/11/202.009
CURRENT FILING DATE: 2005-08-11
PRIOR APPLICATION NUMBER: US/09/989,994
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1284
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-202-009-1284

Query Match 46.3%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GCGGCATCG 15
| | | | | | | |
DB 1 GCGGCGTCG 9

RESULT 17

US-10-962-756A-46
Sequence 46, Application US/10962756A
Publication No. US20050255488A1
GENERAL INFORMATION:
APPLICANT: Aerssens, Jeroen
APPLICANT: Athanasios, Maria
APPLICANT: Brain, Carlos
APPLICANT: Cohen, Nadine
APPLICANT: Dain, Bradley
APPLICANT: Denton, R. Rex
APPLICANT: Judson, Richard S.
APPLICANT: Ozdemir, Vural
APPLICANT: Reed, Carol R.
TITLE OF INVENTION: NTRK1 Genetic Markers Associated with Age of Onset of Alzheimer's
FILE REFERENCE: 2300.0020001
CURRENT APPLICATION NUMBER: US/10/962,756A
CURRENT FILING DATE: 2004-10-13
PRIOR APPLICATION NUMBER: US 60/511,247
PRIOR FILING DATE: 2003-10-15
NUMBER OF SEQ ID NOS: 83
SOFTWARE: PatentIn version 3.0
SEQ ID NO 46
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Reverse Primer Extension Oligonucleotides for Detecting Alleles a

OTHER INFORMATION: t PSs in Haplotypes Comprising Preferred Embodiments of Age of C
OTHER INFORMATION: set Markers I and I
US-10-962-756A-46

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CGGCGCG 10
| | | | | | | |
DB 2 CGGCGCG 8

RESULT 18

US-11-225-686-1640
Sequence 1640, Application US/11225686
Publication No. US20060019349A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/11/225,686
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: US/09/989,994
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1640
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1640

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GCGCGCA 12
| | | | | | | |
DB 3 GCGCGCA 9

RESULT 19

US-11-225-686-1641
Sequence 1641, Application US/11225686
Publication No. US20060019349A1
GENERAL INFORMATION:
APPLICANT: LIU, Qiang
TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
FILE OF INVENTION: TRIPLETS BY ZINC FINGERS
FILE REFERENCE: 8325-0011.20 / S11-US2
CURRENT APPLICATION NUMBER: US/11/225,686
CURRENT FILING DATE: 2005-09-12
PRIOR APPLICATION NUMBER: US/09/989,994
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 4085
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1641
LENGTH: 10
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: example target
US-11-225-686-1641

Query Match 43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Job time : 0.001 secs

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QY      6  GCGCGCA 12
      |||||
Db      3  GCGCGCA 9

RESULT 20
US-11-202-009-1640
; Sequence 1640, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1640
Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  GCGCGCA 12
      |||||
Db      3  GCGCGCA 9

RESULT 21
US-11-202-009-1641
; Sequence 1641, Application US/11202009
; Publication No. US20060024726A1
; GENERAL INFORMATION:
; APPLICANT: LIU, Qiang
; TITLE OF INVENTION: POSITION DEPENDENT RECOGNITION OF GNN NUCLEOTIDE
; TITLE OF INVENTION: TRIPLETS BY ZINC FINGERS
; FILE REFERENCE: 8325-0011.20 / S11-US2
; CURRENT APPLICATION NUMBER: US/11/202,009
; CURRENT FILING DATE: 2005-08-11
; PRIOR APPLICATION NUMBER: US/09/989,994
; PRIOR FILING DATE: 2001-11-20
; NUMBER OF SEQ ID NOS: 4085
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1641
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: example target
; OTHER INFORMATION: DNA
US-11-202-009-1641
Query Match      43.8%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 9.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6  GCGCGCA 12
      |||||
Db      3  GCGCGCA 9

Search completed: May 9, 2006, 16:49:14
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November 2005

Published_Applications Nucleic Acid and Published_Applications Amino Acid database searches now generate two sets of results each. The Published_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published_Applications_New databases: older published applications make up the Published_Applications_Main databases.

Searches run against Nucleic Acid Published_Applications produce two sets of results, with the extensions **.rnpbm** (Published_Applications_NA_Main) and **.rnpbn** (Published_Applications_NA_New).
Searches run against Amino Acid Published_Applications produce two sets of results, with the extensions **.rapbm** (Published_Applications_AA_Main) and **.rapbn** (Published_Applications_AA_New).

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RESULT 2
US-09-904-968A-1
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHARDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

;
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25501
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-25501

Query Match 71.7%; Score 20.8; DB 5; Length 728;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGACCTGG 24
DB 173 CCTCCACCTGCTGTGACCTTG 196

RESULT 7
US-10-027-632-25501
; Sequence 25501, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 25501
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-25501

Query Match 71.7%; Score 20.8; DB 6; Length 728;
Best Local Similarity 91.7%; Pred. No. 33;
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGACCTGG 24
DB 173 CCTCCACCTGCTGTGACCTTG 196

RESULT 8
US-09-925-065A-589532/c
; Sequence 589532, Application US/09925065A

;
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589532
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589532

Query Match 71.0%; Score 20.6; DB 4; Length 551;
Best Local Similarity 85.2%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGACCTGTAAT 29
DB 403 ATTCACCTCTGTGTGACCTTGAAAT 377

RESULT 9
US-09-925-065A-589533/c
; Sequence 589533, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589533
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589533

Query Match 71.0%; Score 20.6; DB 4; Length 551;
Best Local Similarity 85.2%; Pred. No. 39;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGACCTGTAAT 29
DB 403 ATTCACCTCTGTGTGACCTTGAAAT 377

RESULT 10
US-09-065A-256045/c
; Sequence 256045, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256045
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256045

Query Match 70.3%; Score 20.4; DB 4; Length 598;
Best Local Similarity 95.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||||| ||||||| |||||||

Db 561 CCTCCTGCTGTGTGACCTGGTA 540

RESULT 11
US-09-925-065A-256046/c
; Sequence 256046, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256046
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256046

Query Match 70.3%; Score 20.4; DB 4; Length 598;
Best Local Similarity 95.5%; Pred. No. 49;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||||| ||||||| |||||||

Db 561 CCTCCTGCTGTGTGACCTGGTA 540

RESULT 12
US-09-925-065A-935980/c
; Sequence 935980, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935980
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935980

Query Match 69.7%; Score 20.2; DB 4; Length 610;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TCCACCTGCTGTGTGACCTGTAA 28
||||| ||||||| ||||||| |||||||

Db 87 TCCAACTACTGTGTGACCTGGAAA 63

RESULT 13
US-09-925-065A-935981/c
; Sequence 935981, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935981
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935981

Query Match 69.7%; Score 20.2; DB 4; Length 610;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Query Match	69.7%	Score 20.2;	DB 4;	Length 639;
Best Local Similarity	88.0%	Pred. No. 60;		
Matches 22; Conservative	0;	Mismatches 3;	Indels 0;	Gaps 0;

Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
Db 607 TGCACCTGCTGTGTGACCTTCTAAA 631

Search completed: May 9, 2006, 06:18:44
Job time : 704.122 secs

Qy 4 TCCACCTGCTGTGTGACCTGGTAA 28
 |||||
Db 87 TCCAACACTGTGTGACCTGGGAAA 63

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RESULT 14
US-09-925-065A-541706
; Sequence 541706, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289, 846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541706
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-541706

```

```
Query Match      69.7%; Score 20.2; DB 4; Length 639;
Best Local Similarity 88.0%; Pred. No. 60;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
 |
Dβ 607 TGCACCTGCTGTGTGACCTTCTAAA 631

```

RESULT 15
US-09-925-065A-541707
; Sequence 541707, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 541707
; LENGTH: 639
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-541707

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:37:24 ; Search time 656.044 Seconds
(without alignments)
180.024 Million cell updates/sec

Title: US-09-904-968A-3

Perfect score: 29

Sequence: 1 ccattccactgctgtgacctggttaaat 29

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA New.*
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2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq.*
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4: /SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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6: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq.*
7: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq1.*
8: /SIDSS/ptodata/1/pubpna/US09_NEW_PUB.seq2.*
9: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq.*
10: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq1.*
11: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq2.*
12: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq3.*
13: /SIDSS/ptodata/1/pubpna/US10_NEW_PUB.seq4.*
14: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq.*
15: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq2.*
16: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq3.*
17: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq4.*
18: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq5.*
19: /SIDSS/ptodata/1/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21.6	74.5	1094	10	US-10-750-185-40770
2	21.6	74.5	1094	10	US-10-750-623-40770
3	21	72.4	336	7	US-09-925-065A-336757
4	21	72.4	339	7	US-09-925-065A-612157
5	21	72.4	345	12	US-10-301-480-410051
6	21	72.4	345	12	US-10-301-480-1023460
7	20.6	71.0	551	7	US-09-925-065A-589532
8	20.6	71.0	551	7	US-09-925-065A-589533
9	20.4	70.3	598	7	US-09-925-065A-256045
10	20.4	70.3	598	7	US-09-925-065A-256046
11	20.4	70.3	609	12	US-10-301-480-334798
12	20.4	70.3	609	12	US-10-301-480-334799
13	20.4	70.3	609	12	US-10-301-480-948207
14	20.4	70.3	609	12	US-10-301-480-948208

c 15	20.2	69.7	610	7	US-09-925-065A-935980	Sequence 935980,
c 16	20.2	69.7	610	7	US-09-925-065A-935981	Sequence 935981,
c 17	20.2	69.7	639	7	US-09-925-065A-541706	Sequence 541706,
18	20.2	69.7	639	7	US-09-925-065A-541707	Sequence 541707,
19	20.2	69.7	13667	17	US-11-128-061-1065	Sequence 1065, Ap
20	20.2	69.7	13667	17	US-11-128-049-1065	Sequence 1065, Ap
21	20	69.0	201	10	US-10-995-561-65184	Sequence 65184, A
22	20	69.0	528	12	US-10-301-480-372169	Sequence 372169,
23	20	69.0	528	12	US-10-301-480-985578	Sequence 985578,
c 24	20	69.0	530	7	US-09-925-065A-295310	Sequence 295310,
c 25	20	69.0	557	7	US-09-925-065A-295309	Sequence 295309,
26	20	69.0	557	12	US-10-301-480-372168	Sequence 372168,
27	20	69.0	557	12	US-10-301-480-985577	Sequence 985577,
c 28	20	69.0	601	7	US-09-925-065A-884195	Sequence 884195,
c 29	20	69.0	601	7	US-09-925-065A-910370	Sequence 910370,
c 30	20	69.0	601	7	US-09-925-065A-910371	Sequence 910371,
c 31	20	69.0	605	7	US-09-925-065A-327159	Sequence 327159,
c 32	20	69.0	606	12	US-10-301-480-401205	Sequence 401205,
c 33	20	69.0	606	12	US-10-301-480-1014614	Sequence 1014614,
34	20	69.0	659	7	US-09-925-065A-785405	Sequence 785405,
35	20	69.0	659	7	US-09-925-065A-785406	Sequence 785406,
c 36	20	69.0	1050	10	US-10-750-185-50274	Sequence 50274, A
c 37	20	69.0	1050	10	US-10-750-623-50274	Sequence 50274, A
38	20	69.0	66916	10	US-10-995-561-13374	Sequence 13374, A
39	19.8	68.3	25667	11	US-10-330-773-422	Sequence 422, App
40	19.8	68.3	139573	12	US-10-506-513-3	Sequence 3, Appli
41	19.6	67.6	201	17	US-11-124-367A-24332	Sequence 24332, A
42	19.6	67.6	443	7	US-09-925-065A-463434	Sequence 463434,
43	19.6	67.6	590	7	US-09-925-065A-223323	Sequence 223323,
44	19.6	67.6	599	12	US-10-301-480-308284	Sequence 308284,
45	19.6	67.6	599	12	US-10-301-480-921693	Sequence 921693,

ALIGNMENTS

RESULT 1
US-10-750-185-40770
; Sequence 40770, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MW1100-2
; CURRENT APPLICATION NUMBER: US/10750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40770
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine 19866881093594
US-10-750-185-40770

Query Match 74.5%; Score 21.6; DB 10; Length 1094;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 CCATCCACTGCTGTGTCACCTGGTAA 28
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Db 1053 CCATCCACCAGCTGTGTCACCTGAGAA 1080
|||||

RESULT 2
US-10-750-623-40770

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; Sequence 40770, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: Denise, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 40770
; LENGTH: 1094
; TYPE: DNA
; ORGANISM: Bovine 19866881093594
US-10-750-623-40770

Query Match 74.5%; Score 21.6; DB 10; Length 1094;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 24; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAA 28
Db 1053 CCATTACCACGCTGTGTGACCTGGAGAA 1080

RESULT 3
US-09-925-065A-336757
; Sequence 336757, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 336757
; LENGTH: 336
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-336757

Query Match 72.4%; Score 21; DB 7; Length 336;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
Db 263 CCACCCACTAGTGTGTGACCTGGGAAAT 291

RESULT 4
US-09-925-065A-612157/c
; Sequence 1023460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410051
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-410051

Query Match 72.4%; Score 21; DB 12; Length 345;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
Db 263 CCACCCACTAGTGTGTGACCTGGGAAAT 291

RESULT 6
US-10-301-480-1023460
; Sequence 1023460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 410051
; LENGTH: 345
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-410051

Query Match 72.4%; Score 21; DB 12; Length 345;
Best Local Similarity 82.8%; Pred. No. 20;
Matches 24; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCATCCACCTGCTGTGTGACCTGGTAAAT 29
Db 263 CCACCCACTAGTGTGTGACCTGGGAAAT 291

RESULT 6
US-10-301-480-1023460
; Sequence 1023460, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 589533
; LENGTH: 551
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-589533

Query Match          71.0%; Score 20.6; DB 7; Length 551;
Best Local Similarity 85.2%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCCACCTGCTGTGTGACCTGGTAAAT 29
   ||||| ||||| ||||| |||||
DB 403 ATTCACCTTCTGTGTGACCTTGGAAAT 377

RESULT 9
US-09-925-065A-256045/c
; Sequence 256045, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256045
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256045

Query Match          70.3%; Score 20.4; DB 7; Length 598;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
   ||||| ||||| ||||| |||||
DB 561 CTTCTCTGCTGTGTGACCTGGTA 540

RESULT 10
US-09-925-065A-256046/c
; Sequence 256046, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 256046
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-256046
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```
Query Match 70.3%; Score 20.4; DB 7; Length 598;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 561 CCTCCTGCTGTGTGACCTGGTA 540
```

```
RESULT 11
US-10-301-480-334798/c
; Sequence 334798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334798
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-334798
```

```
Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539
```

```
RESULT 12
US-10-301-480-334799/c
; Sequence 334799, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
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```
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334799
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-334799
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Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539
```

```
RESULT 13
US-10-301-480-948207/c
; Sequence 948207, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 948207
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-948207
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Query Match 70.3%; Score 20.4; DB 12; Length 609;
Best Local Similarity 95.5%; Pred. No. 40;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CCACCTGCTGTGTGACCTGGTA 26
||| ||||| ||||| ||||| |||||
Db 560 CCTCCTGCTGTGTGACCTGGTA 539
```

```
RESULT 14
US-10-301-480-948208/c
; Sequence 948208, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
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```

; SEQ ID NO 948208
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo
US-10-301-480-948208

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Query Match	70.3%	Score 20.4;	DB 12;	Length 609;
Best Local Similarity	95.5%	Pred. No. 40;		
Matches 21; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

Qy 5 CCACCTGCTGTGTGACCTGGTA 26
Db 560 CCTCCTGCTGTGTGACCTGGTA 539

RESULT 15

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US-09-925-065A-935980/c
; Sequence 935980, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 935980
; LENGTH: 610
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-935980

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```
Query Match      69.7%; Score 20.2; DB 7; Length 610;
Best Local Similarity 88.0%; Pred. No. 49;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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Qy 4 TCCACCTGCTGTGTGACCTGGTAAA 28
 ||||| || |
Dδ 87 TCCAACTACTGTGTGACCTGGGAA 63

Search completed: May 9, 2006, 06:39:10
Job time : 656.044 secs

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GenCore version 5.1.8
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 71.6444 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-4

Perfect score: 26
Sequence: 1 ccactctatcgcccttctaagcat 26

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
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3: /cgn2_6/prodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/prodata/1/ina/H_COMB.seq.*
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7: /cgn2_6/prodata/1/ina/PP_COMB.seq.*
8: /cgn2_6/prodata/1/ina/RE_COMB.seq.*
9: /cgn2_6/prodata/1/ina/backfiles1.seq.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	31571	2	US-08-323-443B-1
2	26	100.0	53526	3	US-08-658-136-2
3	26	100.0	53577	3	US-08-658-136-1
4	26	100.0	53577	3	US-08-460-218A-1
5	19.6	75.4	4403765	3	US-09-103-840A-2
6	19.6	75.4	4411529	3	US-09-103-840A-1
7	18.2	70.0	601	3	US-09-949-016-27337
8	18.2	70.0	601	3	US-09-949-016-63547
9	18.2	70.0	24709	3	US-09-949-016-12225
10	18.2	70.0	24710	3	US-09-949-016-13595
11	18.2	70.0	213456	3	US-09-820-007-3
12	18.2	70.0	323820	3	US-09-949-016-14139
13	18	69.2	143	3	US-09-513-999C-25080
14	18	69.2	27272	3	US-09-949-016-15737
15	18	69.2	32177	3	US-09-949-002-712
16	17.8	68.5	601	3	US-09-949-016-82906
17	17.8	68.5	32998	3	US-09-408-020-1
18	17.6	67.7	8000	3	US-09-415-784-101
19	17.6	67.7	8000	3	US-09-415-784-102
20	17.6	67.7	8000	3	US-09-415-785A-101
21	17.6	67.7	8000	3	US-09-415-785A-102
22	17.6	67.7	8000	3	US-08-944-465-101
23	17.6	67.7	8000	3	US-08-944-465-102
24	17.6	67.7	8000	3	US-09-415-868-101

25	17.6	67.7	8000	3	US-09-415-868-101	Sequence 102, App
26	17.6	67.7	8000	3	US-09-415-900-101	Sequence 101, App
27	17.6	67.7	8000	3	US-09-415-900-102	Sequence 102, App
28	17.6	67.7	8000	3	US-09-507-362-101	Sequence 101, App
29	17.6	67.7	8000	3	US-09-507-362-102	Sequence 102, App
30	17.6	67.7	9951	3	US-09-193-707-3	Sequence 3, Appli
31	17.6	67.7	10524	3	US-09-193-707-4	Sequence 4, Appli
32	17.6	67.7	11282	3	US-09-733-042-1	Sequence 1, Appli
33	17.6	67.7	11703	2	US-08-801-263A-8	Sequence 8, Appli
34	17.6	67.7	11703	3	US-09-102-248-8	Sequence 8, Appli
35	17.6	67.7	11703	3	US-09-367-764-8	Sequence 8, Appli
36	17.6	67.7	11740	3	US-09-415-784-103	Sequence 103, App
37	17.6	67.7	11740	3	US-09-415-785A-103	Sequence 103, App
38	17.6	67.7	11740	3	US-08-944-465-103	Sequence 103, App
39	17.6	67.7	11740	3	US-09-415-868-103	Sequence 103, App
40	17.6	67.7	11740	3	US-09-415-900-103	Sequence 103, App
41	17.6	67.7	11740	3	US-09-507-362-103	Sequence 103, App
42	17.6	67.7	11927	3	US-09-193-707-5	Sequence 5, Appli
43	17.6	67.7	13905	3	US-08-972-218-1	Sequence 1, Appli
44	17.6	67.7	13905	3	US-09-193-707-1	Sequence 1, Appli
45	17.6	67.7	16656	2	US-08-741-881-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-323-443B-1
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323.443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 26; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATGCGCCCTTCTTAAGCAT 26
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Db 2619 CCACCTCATGCGCCCTTCTTAAGCAT 2644

RESULT 2
US-08-658-136-2/c
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 26; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATGCGCCCTTCTTAAGCAT 26
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Db 4314 CCACCTCATGCGCCCTTCTTAAGCAT 4289

RESULT 4
US-08-460-215A-1/c
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 26; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTTAAGCAT 26
Db 4314 CCACCTCATCGCCCTTCTTAAGCAT 4289

RESULT 5
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 75.4%; Score 19.6; DB 3; Length 4403765;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTTAAGCAT 26
Db 3008548 CCACCTCATCGCCCTTCTTAAGCAT 3008573

RESULT 6
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.

; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 75.4%; Score 19.6; DB 3; Length 4411529;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTTAAGCAT 26
Db 3013643 CCACCTCATCGCCCTTCTTAAGCAT 3013668

RESULT 7
US-09-949-016-27337
; Sequence 27337, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27337
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-27337

Query Match 70.0%; Score 18.2; DB 3; Length 601;
Best Local Similarity 87.0%; Pred. No. 48;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCTTAAGCA 25
Db 362 ACCTTAGCCCTTCTTCAGCA 384

RESULT 8
US-09-949-016-63547
; Sequence 63547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20

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; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63547
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-63547

Query Match
Best Local Similarity 70.0%; Score 18.2; DB 3; Length 601;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCA 25
||||| ||||| ||||| |||||
Db 362 ACCTCTTAGCCCTTCCTCAGCA 384

RESULT 9
US-09-949-016-12225
; Sequence 12225, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12225
; LENGTH: 24709
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12225

Query Match
Best Local Similarity 70.0%; Score 18.2; DB 3; Length 24709;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCA 25
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Db 19303 ACCTCTTAGCCCTTCCTCAGCA 19325

RESULT 10
US-09-949-016-13595
; Sequence 13595, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13595
; LENGTH: 24710
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13595

Query Match
Best Local Similarity 70.0%; Score 18.2; DB 3; Length 24710;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCA 25
||||| ||||| ||||| |||||
Db 19303 ACCTCTTAGCCCTTCCTCAGCA 19325

RESULT 11
US-09-820-007-3
; Sequence 3, Application US/09820007
; Patent No. 6830900
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1) - (213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match
Best Local Similarity 70.0%; Score 18.2; DB 3; Length 213456;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTCCTAAGCAT 26
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Db 184770 CCTCATCATCTCTTCCAAAGCAT 184792

RESULT 12
US-09-949-016-14139
; Sequence 14139, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14139
; LENGTH: 323820
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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; NAME/KEY: misc.feature
; LOCATION: (1)...(323820)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14139

Query Match 70.0%; Score 18.2; DB 3; Length 323820;
Best Local Similarity 87.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTCTCTAAGCAT 26
|||||
Db 184486 CCTCATCTCTCTCCAAAGCAT 184508

RESULT 13
US-09-513-999C-25080/c
; Sequence 25080, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 25080
; LENGTH: 143
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-513-999C-25080

Query Match 69.2%; Score 18; DB 3; Length 143;
Best Local Similarity 80.8%; Pred. No. 47;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTCTAAGCAT 26
|||||
Db 118 CCACCCCATCCGCCCCACCTCAGCAT 93

RESULT 14
US-09-949-016-15737
; Sequence 15737, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15737
; LENGTH: 27727
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15737

Query Match 69.2%; Score 18; DB 3; Length 27727;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 CCACCTCATCGCCCTTCTCTAAGCAT 26
|||||
Db 16542 CCACCTCAGGACCTTCCCAAGCTT 16567

RESULT 15
US-09-949-002-712/c
; Sequence 712, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 712
; LENGTH: 32177
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(32177)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-002-712

Query Match 69.2%; Score 18; DB 3; Length 32177;
Best Local Similarity 80.8%; Pred. No. 1.1e+02;
Matches 21; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCTCTAAGCAT 26
|||||
Db 3200 CCACCTCTCCACCTCTCTAAGCCT 3175

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Job time : 78.6444 secs

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OM nucleic - nucleic search, using sw model

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(without alignments)
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Title: US-09-904-968A-4

Perfect score: 26

Sequence: 1 ccacctcatcgcccttctaagcat 26

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Maximum Match 100%

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- 5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	100.0	26	3	US-09-904-968A-4
2	26	100.0	53522	3	US-09-904-968A-1
3	24.4	93.8	6423	6	US-10-240-485-121
4	19.6	75.4	80264	9	US-10-737-318-83
5	18.8	72.3	796	7	US-10-424-599-7186
6	18.2	70.0	537	4	US-09-925-065A-49324
7	18.2	70.0	537	4	US-09-925-065A-49325
8	18.2	70.0	569	4	US-09-925-065A-262314
9	18.2	70.0	569	4	US-09-925-065A-437738
10	18.2	70.0	569	4	US-09-925-065A-437739
11	18.2	70.0	569	4	US-09-925-065A-437740
12	18.2	70.0	5549	3	US-09-764-877-2860
13	18.2	70.0	5549	3	US-10-242-515-2860
14	18.2	70.0	58952	5	US-10-087-192-1890
15	18.2	70.0	213456	3	US-09-820-007-3
16	18.2	70.0	213456	3	US-10-981-724-3
17	18	69.2	352	8	US-10-357-930-59953
18	18	69.2	554	8	US-10-357-930-60566
19	18	69.2	575	4	US-09-925-065A-471791
20	18	69.2	631	7	US-10-437-963-97251
21	18	69.2	846	5	US-10-027-632-152758
22	18	69.2	846	6	US-10-027-632-152758
23	18	69.2	40000	8	US-10-741-600-18014

C 24	18	69.2	44990	7	US-10-052-482-217	Sequence 217, App
C 25	17.8	68.5	537	4	US-09-925-065A-49323	Sequence 49323, A
C 26	17.8	68.5	567	4	US-09-925-065A-590403	Sequence 590403, A
C 27	17.8	68.5	569	4	US-09-925-065A-437741	Sequence 437741, A
C 28	17.8	68.5	32998	5	US-10-027-806-1	Sequence 1, Appli
C 29	17.8	68.5	32998	5	US-10-034-623-1	Sequence 1, Appli
C 30	17.8	68.5	32998	5	US-10-027-801-1	Sequence 1, Appli
C 31	17.8	68.5	32998	6	US-10-029-120-1	Sequence 1, Appli
C 32	17.6	67.7	199	3	US-09-294-0938-4296	Sequence 4296, Ap
C 33	17.6	67.7	200	3	US-09-922-293-1399	Sequence 1399, Ap
C 34	17.6	67.7	256	6	US-10-029-386-14670	Sequence 14670, A
C 35	17.6	67.7	267	8	US-10-425-115-175164	Sequence 175164, A
C 36	17.6	67.7	287	3	US-09-922-293-1398	Sequence 1398, Ap
C 37	17.6	67.7	533	6	US-10-029-386-967	Sequence 967, App
C 38	17.6	67.7	754	8	US-09-925-065A-502013	Sequence 502013, A
C 39	17.6	67.7	754	8	US-10-425-115-84140	Sequence 84140, A
C 40	17.6	67.7	1089	9	US-10-343-477A-47	Sequence 47, Appl
C 41	17.6	67.7	1759	8	US-10-739-930-4071	Sequence 4071, Ap
C 42	17.6	67.7	1865	8	US-10-739-930-5444	Sequence 5444, Ap
C 43	17.6	67.7	8000	3	US-09-507-362-101	Sequence 101, App
C 44	17.6	67.7	8000	3	US-09-507-362-102	Sequence 102, App
C 45	17.6	67.7	8000	6	US-10-391-441-101	Sequence 101, App

ALIGNMENTS

RESULT 1

US-09-904-968A-4
; Sequence 4, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHANDEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: PCR primer BPR9
US-09-904-968A-4

Query Match 100.0%; Score 26; DB 3; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26

Db 1 CCACCTCATCGCCCTTCCTAAGCAT 26

RESULT 2

US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHANDEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

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; FILE REFERENCE: JHUI680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1
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Query Match 100.0%; Score 26; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
Db 4315 CCACCTCATCGCCCTTCCTAAGCAT 4290
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RESULT 3

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US-10-240-485-121/c
; Sequence 121, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; TITLE OF INVENTION: Metastasis
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 121
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-121
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Query Match 93.8%; Score 24.4; DB 6; Length 6423;
Best Local Similarity 96.2%; Pred. No. 0.28;
Matches 25; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
Db 5876 CCACCTCATCGCCCTTCCTAAGCAT 5851
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RESULT 4

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US-10-737-318-83/c
; Sequence 83, Application US/10737318
; Publication No. US20050202442A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Malandro, Marc S.
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER
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; FILE REFERENCE: 529452002800
; CURRENT APPLICATION NUMBER: US/10/737,318
; CURRENT FILING DATE: 2003-12-15
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 80264
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)---(80264)
; OTHER INFORMATION: n = A,T,C or G
US-10-737-318-83
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Query Match 75.4%; Score 19.6; DB 9; Length 80264;
Best Local Similarity 84.6%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
Db 7141 CAACCTCCACTCCCTTCCTAAGCAT 7116
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RESULT 5

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US-10-424-599-7186
; Sequence 7186, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 7186
; LENGTH: 796
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_106497C.1
US-10-424-599-7186
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Query Match 72.3%; Score 18.8; DB 7; Length 796;
Best Local Similarity 90.9%; Pred. No. 99;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 CCACCTCATCGCCCTTCCTAA 22
Db 731 CCACCTCATCGCACTTCCAA 752
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RESULT 6

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US-09-925-065A-49324/c
; Sequence 49324, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
```

; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49324
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49324

Query Match 70.0%; Score 18.2; DB 4; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCTTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 124 CACCTCTCGCCCTCTCTCAGC 102

RESULT 7

US-09-925-065A-49325/c
; Sequence 49325, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49325
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49325

Query Match 70.0%; Score 18.2; DB 4; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCTTAAGC 24
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Db 124 CACCTCTCGCCCTCTCTCAGC 102

RESULT 8

US-09-925-065A-262314
; Sequence 262314, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262314
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-262314

Query Match 70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCTTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 9

US-09-925-065A-437738
; Sequence 437738, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437738
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437738

Query Match 70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCTTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 10

US-09-925-065A-437739
; Sequence 437739, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08

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; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437739
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437739
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Query Match 70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 495 CACCTCTCGCCCTTCCTCAGC 517
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RESULT 11
US-09-925-065A-437740
; Sequence 437740, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437740
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437740
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Query Match 70.0%; Score 18.2; DB 4; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 495 CACCTCTCGCCCTTCCTCAGC 517
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```
RESULT 12
US-09-764-877-2860
; Sequence 2860, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
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; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2860
; LENGTH: 5549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-877-2860
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Query Match 70.0%; Score 18.2; DB 3; Length 5549;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 CACCTCATCGCCCTTCCTAAGC 24
||||| ||||| ||||| ||||| |||||
Db 2510 CACCTCTCGCCCTTCCTCAGC 2532
```

```
RESULT 13
US-10-242-515-2860
; Sequence 2860, Application US/10242515
; Publication No. US20040009488A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005C1
; CURRENT APPLICATION NUMBER: US/10/242,515
; CURRENT FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: 09/764,877
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: 60/179,065
; PRIOR FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/180,628
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: 60/214,886
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/217,487
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,758
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/220,963
; PRIOR FILING DATE: 2000-07-26
; PRIOR APPLICATION NUMBER: 60/217,496
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 60/225,447
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/218,290
; PRIOR FILING DATE: 2000-07-14
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2860
; LENGTH: 5549
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-242-515-2860
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Query Match 70.0%; Score 18.2; DB 6; Length 5549;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 2510 CACCTCTCGCCCTTCCTCAGC 2532
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RESULT 14
US-10-087-192-1690
; Sequence 1690, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
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; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1690
; LENGTH: 58952
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(58952)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1690

Query Match 70.0%; Score 18.2; DB 5; Length 58952;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCACCTCATCGCCCTTCCTAAG 23
Db 30297 CCACCCCACTCCCTTCCTAAG 30319

RESULT 15
US-09-820-007-3
; Sequence 3, Application US/09820007
; Publication No. US20040229304A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CL001205
; CURRENT APPLICATION NUMBER: US/09/820,007
; CURRENT FILING DATE: 2001-03-29
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 213456
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(213456)
; OTHER INFORMATION: n = A,T,C or G
US-09-820-007-3

Query Match 70.0%; Score 18.2; DB 3; Length 213456;
Best Local Similarity 87.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 CCTCATCGCCCTTCCTAAGCAT 26
Db 184770 CCTCATCACTCTTCCTCAAGCAT 184792

Search completed: May 9, 2006, 06:18:30
Job time : 631.489 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:37:24 ; Search time 588.178 Seconds
(without alignments)
180.024 Million cell updates/sec

Title: US-09-904-968A-4

Perfect score: 26
Sequence: 1 ccacctcatgcccttcctaagcat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9305428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA_New.*

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2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq.*
3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	19.2	73.8	11 US-10-932-182A-3010	Sequence 3010, Ap
2	19.2	73.8	11 US-10-932-182A-3010	Sequence 3010, Ap
3	19.2	73.8	90739 11 US-10-330-773-902	Sequence 902, App
4	18.2	70.0	537 7 US-09-925-065A-49324	Sequence 49324, A
5	18.2	70.0	537 7 US-09-925-065A-49325	Sequence 49325, A
6	18.2	70.0	537 11 US-10-301-480-150562	Sequence 150562, A
7	18.2	70.0	537 11 US-10-301-480-150563	Sequence 150563, A
8	18.2	70.0	537 12 US-10-301-480-763971	Sequence 763971, A
9	18.2	70.0	537 12 US-10-301-480-763972	Sequence 763972, A
10	18.2	70.0	569 7 US-09-925-065A-262314	Sequence 262314, A
11	18.2	70.0	569 7 US-09-925-065A-437738	Sequence 437738, A
12	18.2	70.0	569 7 US-09-925-065A-437739	Sequence 437739, A
13	18.2	70.0	569 7 US-09-925-065A-437740	Sequence 437740, A
14	18.2	70.0	572 12 US-10-301-480-340535	Sequence 340535, A

15	18.2	70.0	572 12 US-10-301-480-499114	Sequence 499114, A
16	18.2	70.0	572 12 US-10-301-480-499115	Sequence 499115, A
17	18.2	70.0	572 12 US-10-301-480-953944	Sequence 953944, A
18	18.2	70.0	572 12 US-10-301-480-1112523	Sequence 1112523, A
19	18.2	70.0	572 12 US-10-301-480-1112524	Sequence 1112524, A
20	18	69.2	575 7 US-09-925-065A-471791	Sequence 471791, A
21	18	69.2	1068 10 US-10-750-185-39158	Sequence 39158, A
22	18	69.2	1068 10 US-10-750-623-39158	Sequence 39158, A
23	18	69.2	1673 10 US-10-750-185-47820	Sequence 47820, A
24	18	69.2	1673 10 US-10-750-623-47820	Sequence 47820, A
25	17.8	68.5	537 7 US-09-925-065A-49323	Sequence 49323, A
26	17.8	68.5	537 11 US-10-301-480-150561	Sequence 150561, A
27	17.8	68.5	537 12 US-10-301-480-763970	Sequence 763970, A
28	17.8	68.5	567 7 US-09-925-065A-590403	Sequence 590403, A
29	17.8	68.5	569 7 US-09-925-065A-437741	Sequence 437741, A
30	17.8	68.5	572 12 US-10-301-480-499116	Sequence 499116, A
31	17.8	68.5	572 12 US-10-301-480-1112525	Sequence 1112525, A
32	17.6	67.7	675 7 US-09-925-065A-502013	Sequence 502013, A
33	17.6	67.7	3022 10 US-10-750-185-42216	Sequence 42216, A
34	17.6	67.7	3022 10 US-10-750-623-42216	Sequence 42216, A
35	17.6	67.7	11282 17 US-11-177-504-1	Sequence 1, Appli
36	17.6	67.7	23704 17 US-11-124-368A-2905	Sequence 2905, Ap
37	17.6	67.7	268685 10 US-10-933-025-22	Sequence 22, Appl
38	17.6	67.7	268685 18 US-11-219-360-22	Sequence 22, Appl
39	17.2	66.2	459 7 US-09-925-065A-447393	Sequence 447393, A
40	17.2	66.2	2937 10 US-10-750-185-60052	Sequence 60052, A
41	17.2	66.2	2937 10 US-10-750-623-60052	Sequence 60052, A
42	17	65.4	390 9 US-10-511-937-552	Sequence 552, App
43	17	65.4	457 12 US-10-301-480-379405	Sequence 379405, A
44	17	65.4	457 12 US-10-301-480-992814	Sequence 992814, A
45	17	65.4	458 7 US-09-925-065A-303251	Sequence 303251, A

ALIGNMENTS

RESULT 1

US-10-932-182A-3010
; Sequence 3010, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3010
; LENGTH: 1872
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3010

Query Match 73.8% ; Score 19.2 ; DB 11 ; Length 1872 ;
Best Local Similarity 87.5% ; Pred. No. 42 ;
Matches 21 ; Conservative 0 ; Mismatches 3 ; Indels 0 ; Gaps 0 ;

Qy 1 CCACCTCATGCCCTTCCTTAAGC 24

Db 664 CCACCTCATGCCCTTCCTTAAGC 687

RESULT 2

US-10-932-182A-3010
; Sequence 3010, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO

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; APPLICANT: NAKAMURA, NORIHA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
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; TYPE: DNA
; LENGTH: 1872
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-3010

Query Match      73.8%; Score 19.2; DB 11; Length 1872;
Best Local Similarity 87.5%; Pred. No. 42;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCCTTCCTAAGC 24
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Db 664 CCACCTCATCGCCCTTCCTCAACC 687

RESULT 3
US-10-330-773-902
; Sequence 902, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902
; LENGTH: 90739
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(90739)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-902

Query Match      73.8%; Score 19.2; DB 11; Length 90739;
Best Local Similarity 87.5%; Pred. No. 58;
Matches 21; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 ACCTCATCGCCCTTCCTAAGCAT 26
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Db 68646 ACCTCATCACCCCTTCCTCTGCAT 68669

RESULT 4
US-09-925-065A-49324/c
; Sequence 49324, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
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; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49324
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49324

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Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 124 CACCTCTCGCCCTTCCTCAGC 102

RESULT 5
US-09-925-065A-49325/c
; Sequence 49325, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 49325
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-49325

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Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 124 CACCTCTCGCCCTTCCTCAGC 102

RESULT 6
US-10-301-480-150562/c
; Sequence 150562, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
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; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150562
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-150562

Query Match 70.0%; Score 18.2; DB 11; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 124 CACCTCTCGCCCTCCTCAGC 102

RESULT 7

US-10-301-480-150563/c
; Sequence 150563, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 150563
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-150563

Query Match 70.0%; Score 18.2; DB 11; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 124 CACCTCTCGCCCTCCTCAGC 102

RESULT 8

US-10-301-480-763971/c
; Sequence 763971, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763971
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-763971

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Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 124 CACCTCTCGCCCTCCTCAGC 102

RESULT 9

US-10-301-480-763972/c
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; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 763972
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-763972

Query Match 70.0%; Score 18.2; DB 12; Length 537;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 124 CACCTCTCGCCCTCCTCAGC 102

RESULT 10

US-09-925-065A-262314
; Sequence 262314, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262314
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-262314

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 11

US-09-925-065A-437738
; Sequence 437738, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437738
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437738

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 12

US-09-925-065A-437739
; Sequence 437739, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437739
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437739

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 13

US-09-925-065A-437740
; Sequence 437740, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 437740
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-437740

Query Match 70.0%; Score 18.2; DB 7; Length 569;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
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Db 495 CACCTCTCGCCCTCTCTCAGC 517

RESULT 14

US-10-301-480-340535
; Sequence 340535, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 340535
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-340535

Query Match 70.0%; Score 18.2; DB 12; Length 572;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;

Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
|||||
Db 495 CACCTCTCGCCCTCCTCAGC 517

RESULT 15

US-10-301-480-499114
; Sequence 499114, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 499114
; LENGTH: 572
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-499114

Query Match 70.0%; Score 18.2; DB 12; Length 572;
Best Local Similarity 87.0%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CACCTCATCGCCCTTCCTAAGC 24
|||||
Db 495 CACCTCTCGCCCTCCTCAGC 517

Search completed: May 9, 2006, 06:39:10
Job time : 589.178 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:14:10 ; Search time 52.3556 Seconds
(without alignments)
645.083 Million cell updates/sec

Title: US-09-904-968A-19

Perfect score: 19

Sequence: 1 ggtcgcgtgtgtgcgaagg 19

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*
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8: /cgn2_6/ptodata/1/ina/RE COMB.seq.*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	19	100.0	31571	2	US-08-323-443B-1
C 2	19	100.0	53526	3	US-08-658-136-2
C 3	19	100.0	53577	3	US-08-658-136-1
C 4	19	100.0	53577	3	US-08-460-215A-1
C 5	16.4	86.3	906	3	US-09-489-039A-565
C 6	16.4	86.3	954	3	US-09-489-039A-449
C 7	15.8	83.2	780	3	US-09-902-540-5800
C 8	15.8	83.2	858	3	US-09-902-540-8298
C 9	15.8	83.2	6935	3	US-09-902-540-865
C 10	15.8	83.2	72704	3	US-09-902-540-1273
C 11	15.4	81.1	1182	3	US-09-902-540-8004
C 12	15.4	81.1	6439	3	US-09-902-540-813
C 13	15	78.9	633	3	US-08-998-416-1115
C 14	15	78.9	1173	3	US-09-489-039A-1206
C 15	15	78.9	3396	3	US-09-668-680-6
C 16	15	78.9	3423	3	US-09-668-680-7
C 17	14.8	77.9	153	3	US-09-513-999C-32794
C 18	14.8	77.9	278	3	US-09-471-276-696
C 19	14.8	77.9	435	3	US-09-313-294A-2721
C 20	14.8	77.9	601	3	US-09-902-540-8251
C 21	14.8	77.9	601	3	US-09-949-016-139687
C 22	14.8	77.9	601	3	US-09-949-016-139687
C 23	14.8	77.9	1155	3	US-09-902-540-139688
C 24	14.8	77.9	1179	3	US-09-902-540-8018

Sequence 4680, Ap
Sequence 2768, Ap
Sequence 287, App
Sequence 439, App
Sequence 2864, App
Sequence 805, App
Sequence 853, App
Sequence 815, App
Sequence 1230, Ap
Sequence 1240, Ap
Sequence 15691, A
Sequence 595, App
Sequence 66, Appl
Sequence 66, Appl
Sequence 3038, Ap
Sequence 624, App
Sequence 425, App
Sequence 491, App
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli

25 14.8 77.9 2502 3 US-09-902-540-4680
C 26 14.8 77.9 2598 3 US-09-252-991A-2768
C 27 14.8 77.9 2643 3 US-09-614-221A-287
C 28 14.8 77.9 2643 3 US-09-487-558B-439
C 29 14.8 77.9 2790 3 US-09-252-991A-2864
30 14.8 77.9 6134 3 US-09-902-540-805
C 31 14.8 77.9 6492 3 US-09-902-540-853
C 32 14.8 77.9 9053 3 US-09-902-540-1230
C 33 14.8 77.9 24754 3 US-09-902-540-1230
C 34 14.8 77.9 29509 3 US-09-902-540-1240
C 35 14.8 77.9 87039 3 US-09-949-016-15691
C 36 14.4 75.8 317 3 US-09-221-017B-595
C 37 14.4 75.8 1830 3 US-08-969-683A-66
C 38 14.4 75.8 1830 3 US-09-308-207-66
C 39 14.4 75.8 1860 3 US-09-489-039A-3038
C 40 14.4 75.8 2812 3 US-09-620-312D-624
C 41 14.4 75.8 3405 3 US-09-614-221A-425
C 42 14.4 75.8 4430 3 US-09-902-540-491
C 43 14.4 75.8 15872 3 US-09-105-537-1
C 44 14.4 75.8 15872 3 US-09-091-609-1
C 45 14.4 75.8 15872 3 US-09-091-609-3

ALIGNMENTS

RESULT 1
US-08-323-443B-1/c
; Sequence 1, Application US/08323443B
; Patent No. 5654170
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W.
; APPLICANT: LANDES, GREGORY M.
; APPLICANT: BURN, TIMOTHY C.
; APPLICANT: CONNORS, TIMOTHY D.
; APPLICANT: DACKOWSKI, WILLIAM R.
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, PENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/323,443B
; FILING DATE: 12-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ludwig, S. Peter
; REGISTRATION NUMBER: 25,351
; REFERENCE/DOCKET NUMBER: 0372/0A462
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 527-7700
; TELEFAX: (212) 753-6237
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31571 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens

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; IMMEDIATE SOURCE:
; CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match      100.0%; Score 19; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCGCTGTGGCGAAGG 19
    |||||
Db 3599 GGTCCGCTGTGGCGAAGG 3581

RESULT 2
US-08-658-136-2
; Sequence 2, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-658-136-1

Query Match      100.0%; Score 19; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCCGCTGTGGCGAAGG 19
    |||||
Db 3334 GGTCCGCTGTGGCGAAGG 3352

RESULT 4
US-08-460-215A-1
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,215A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DUGAN, DEBORAH
REGISTRATION NUMBER: 37,315
REFERENCE/DOCKET NUMBER: GENA-17.5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 508-872-8400
TELEFAX: 508-872-5415
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5357 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-460-215A-1

Query Match 100.0%; Score 19; DB 3; Length 53577;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGCGGAAG 19
|||||
DB 3334 GGTCGGCGCTGTGCGGAAG 3352

RESULT 5

US-09-489-039A-565
Sequence 565, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 565
LENGTH: 906
TYPE: DNA

ORGANISM: Klebsiella pneumoniae
US-09-489-039A-565

Query Match 86.3%; Score 16.4; DB 3; Length 906;
Best Local Similarity 94.4%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGCGGAAG 18
|||||
DB 218 GGTCGGCGCTGTGCGGAAG 235

RESULT 6

US-09-489-039A-449/c
Sequence 449, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 449
LENGTH: 954
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-449

Query Match 86.3%; Score 16.4; DB 3; Length 954;
Best Local Similarity 94.4%; Pred. No. 69;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGCGGAAG 18
|||||
DB 725 GGTCGGCGCTGTGCGGAAG 708

RESULT 7

US-09-902-540-5800
Sequence 5800, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B

CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10

NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 5800
LENGTH: 780
TYPE: DNA

ORGANISM: Myxococcus xanthus
US-09-902-540-5800

Query Match 83.2%; Score 15.8; DB 3; Length 780;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGGCGCTGTGCGGAAG 19
|||||
DB 55 GGTCGGCGCTGTGCGGAG 73

RESULT 8

US-09-902-540-8298/c
Sequence 8298, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:

APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof

FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883

PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8298
LENGTH: 858
TYPE: DNA

ORGANISM: Myxococcus xanthus
US-09-902-540-8298

Query Match 83.2%; Score 15.8; DB 3; Length 858;
Best Local Similarity 89.5%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGGCGCTGTGGCGAAGG 19
Db 844 GGTGGCGCTGTGGCGGAGG 826

RESULT 9

US-09-902-540-865
; Sequence 865, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 865
; LENGTH: 6935
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-865

Query Match 83.2%; Score 15.8; DB 3; Length 6935;
Best Local Similarity 89.5%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGGCGCTGTGGCGAAGG 19
Db 16 GGTGGCGCTGTGGCGGAGG 34

RESULT 10

US-09-902-540-1273
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match 83.2%; Score 15.8; DB 3; Length 72704;
Best Local Similarity 89.5%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGGCGCTGTGGCGAAGG 19
Db 65126 GGTGGCGGCTGTGGCGGAGG 65144

RESULT 11

US-09-902-540-8004/c
; Sequence 8004, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8004
; LENGTH: 1182
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8004

Query Match 81.1%; Score 15.4; DB 3; Length 1182;
Best Local Similarity 94.1%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCGAAGG 19
Db 336 TCGCGCTTTGGCGAAGG 320

RESULT 12

US-09-902-540-813
; Sequence 813, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 813
; LENGTH: 6439
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-813

Query Match 81.1%; Score 15.4; DB 3; Length 6439;
Best Local Similarity 94.1%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TCGCGCTGTGGCGAAGG 19
Db 849 TCGCGCTTTGGCGAAGG 865

RESULT 13

US-08-998-416-1115
; Sequence 1115, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippesen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jorgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne

;; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
;; TITLE OF INVENTION: AND USES THEREOF
;; NUMBER OF SEQUENCES: 1152
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: No. 6239264artis Corporation
;; STREET: 3054 Cornwallis Road
;; CITY: Research Triangle Park
;; STATE: No. 6239264th Carolina
;; COUNTRY: USA
;; ZIP: 27709
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/998,416
;; FILING DATE: 24-DEC-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: CH 0016/97
;; FILING DATE: 31-DEC-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Weigle, J. Timothy
;; REGISTRATION NUMBER: 38,241
;; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 919-541-8587
;; TELEFAX: 919-541-8689
;; INFORMATION FOR SEQ ID NO: 1115:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 633 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; ORIGINAL SOURCE:
;; ORGANISM: PAG1180RP
US-08-998-416-1115

Query Match 78.9%; Score 15; DB 3; Length 633;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTGTGGCGAAG 18
|||
Db 119 CGCGCTGTGGCGAAG 133

RESULT 14
US-09-489-039A-1206
; Sequence 1206, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 1206
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1206

Query Match 78.9%; Score 15; DB 3; Length 1173;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CGCGCTGTGGCGAAG 18
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Db 534 CGCGCTGTGGCGAAG 548
RESULT 15
US-09-668-680-6/c
; Sequence 6, Application US/09668680
; Patent No. 6436703
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Zhou, Ping
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Xue, Aidong J.
; APPLICANT: Xu, Chongjun
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6436703el Nucleic Acids and
; FILE REFERENCE: 790CIP2A
; CURRENT APPLICATION NUMBER: US/09/668,680
; CURRENT FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 6
; LENGTH: 3396
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (27)..(2375)
US-09-668-680-6

Query Match 78.9%; Score 15; DB 3; Length 3396;
Best Local Similarity 100.0%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 GCGCTGTGGCGAAG 19
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Db 253 GCGCTGTGGCGAAG 239

Search completed: May 9, 2006, 05:56:09
Job time : 53.3556 secs

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2	19	100.0	53522	3	US-09-904-968A-1	Sequence 1, Appl1	
3	17.4	91.6	623	8	US-10-363-345A-2649	Sequence 2649, Ap	
C	4	17.4	91.6	623	8	US-10-363-345A-2650	Sequence 2650, Ap
5	17.4	91.6	623	9	US-10-363-483A-2649	Sequence 2649, Ap	
C	6	17.4	91.6	623	9	US-10-363-483A-2650	Sequence 2650, Ap
7	17.4	91.6	6423	6	US-10-240-485-121	Sequence 121, App	
8	16.4	86.3	871	7	US-10-437-963-87337	Sequence 87337, A	
9	15.8	83.2	656	7	US-10-437-963-31042	Sequence 31042, A	
10	15.8	83.2	762	6	US-10-369-493-43242	Sequence 43242, A	
11	15.8	83.2	1059	10	US-11-109-593-15	Sequence 15, Appl	
C	12	15.8	83.2	2047	8	US-10-425-115-137211	Sequence 137211,
13	15.8	83.2	5373	10	US-11-097-143-7789	Sequence 7789, Ap	
14	15.8	83.2	67323	10	US-11-109-593-1	Sequence 1, Appl1	
15	15.8	83.2	155350	7	US-10-322-281-691	Sequence 691, App	
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C	17	15.4	81.1	479	7	US-10-767-701-22213	Sequence 22213, A
18	15.4	81.1	1176	6	US-10-369-493-42897	Sequence 42897, A	
C	19	15.4	81.1	1518	5	US-10-116-821-13	Sequence 13, Appl
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C	21	15.4	81.1	1627	7	US-10-425-114-20510	Sequence 20510, A
22	2386	81.1	2386	8	US-10-425-115-120685	Sequence 120685,	
C	23	15.4	81.1	2619	3	US-09-789-561-80	Sequence 80, Appl

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; FILE REFERENCE: JHUI680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

Query Match      100.0%; Score 19; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCCGCGCTGTGGCGAAGG 19
Db 3334 GGTCCGCGCTGTGGCGAAGG 3352

RESULT 3
US-10-363-345A-2649
; Sequence 2649, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2649

Query Match      91.6%; Score 17.4; DB 8; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGCTGTGGCGAAGG 19
Db 196 GGTCCGCGTGTGGCGAAGG 214

RESULT 4
US-10-363-345A-2650/c
; Sequence 2650, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2650
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-345A-2650

Query Match      91.6%; Score 17.4; DB 8; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGCTGTGGCGAAGG 19
Db 428 GGTCCGCGTGTGGCGAAGG 410

RESULT 5
US-10-363-483A-2649
; Sequence 2649, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2649
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-2649

Query Match      91.6%; Score 17.4; DB 9; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGCTGTGGCGAAGG 19
Db 196 GGTCCGCGTGTGGCGAAGG 214

RESULT 6
US-10-363-483A-2650/c
; Sequence 2650, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 2650
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-363-483A-2650

Query Match      91.6%; Score 17.4; DB 9; Length 623;
Best Local Similarity 94.7%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY 1 GGTCCGCGTGTGGCGAAGG 19
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Db 428 GGTCCGCGTGTGGCGAAGG 410

RESULT 7

US-10-240-485-121
; Sequence 121, Application US/10240485
; Publication No. US20030148327A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: FIEFENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with
; FILE REFERENCE: 5013.1007
; CURRENT APPLICATION NUMBER: US/10/240,485
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03970
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 202
; SEQ ID NO 121
; LENGTH: 6423
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-485-121

Query Match 91.6%; Score 17.4; DB 6; Length 6423;
Best Local Similarity 94.7%; Pred. No. 45;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTCCGCGTGTGGCGAAGG 19
|||||
Db 4895 GGTCCGCGTGTGGCGAAGG 4913

RESULT 8

US-10-437-963-87337
; Sequence 87337, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 87337
; LENGTH: 871
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_86292C.1
US-10-437-963-87337

Query Match 86.3%; Score 16.4; DB 7; Length 871;
Best Local Similarity 94.4%; Pred. No. 1.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGCGAAGG 19
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Db 465 GTCGCGCTGTGGCGAAGG 482

RESULT 9

US-10-437-963-31042
; Sequence 31042, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 31042
; LENGTH: 656
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_35387C.1
US-10-437-963-31042

Query Match 83.2%; Score 15.8; DB 7; Length 656;
Best Local Similarity 89.5%; Pred. No. 3.8e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCCGCGTGTGGCGAAGG 19
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Db 625 GGTCCGCGTGTGGCGACGG 643

RESULT 10

US-10-369-493-43242
; Sequence 43242, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 43242
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-10-369-493-43242

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Best Local Similarity 89.5%; Pred. No. 3.7e+02;
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RESULT 11
US-11-109-593-15
; Sequence 15, Application US/11109593
; Publication No. US20050233369A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Ralph
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR JERANGOLIDS
; FILE REFERENCE: 010108.01
; CURRENT APPLICATION NUMBER: US/11/109,593
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,843
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
; LENGTH: 1059
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-109-593-15

Query Match 83.2%; Score 15.8; DB 10; Length 1059;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
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Db 652 GGTCGCGCGTGTGGCGAAGG 670

RESULT 12
US-10-425-115-137211/c
; Sequence 137211, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 137211
; LENGTH: 2047
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_56611C.1
US-10-425-115-137211

Query Match 83.2%; Score 15.8; DB 8; Length 2047;
Best Local Similarity 89.5%; Pred. No. 3.2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
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Db 307 GGTCGCGCAGGGCGCGAAGG 289

RESULT 13
US-11-097-143-7789/c
; Sequence 7789, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:

; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
; TITLE OF INVENTION: DROSOPHILA GENES.
; FILE REFERENCE: CL00728
; CURRENT APPLICATION NUMBER: US/11/097,143
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: 60/157,832
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: 60/160,191
; PRIOR FILING DATE: 1999-10-19
; PRIOR APPLICATION NUMBER: 60/161,932
; PRIOR FILING DATE: 1999-10-28
; PRIOR APPLICATION NUMBER: 60/164,769
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: 60/173,383
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: 60/175,693
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: 60/184,831
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: 60/191,637
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 43008
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7789
; LENGTH: 5373
; TYPE: DNA
; ORGANISM: DROSOPHILA
US-11-097-143-7789

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Best Local Similarity 89.5%; Pred. No. 2.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCGCGCTGTGGCGAAGG 19
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Db 3054 GGACTCGCTGTGGCGAAGG 3036

RESULT 14
US-11-109-593-1
; Sequence 1, Application US/11109593
; Publication No. US20050233369A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Ralph
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: BIOSYNTHETIC GENE CLUSTER FOR JERANGOLIDS
; FILE REFERENCE: 010108.01
; CURRENT APPLICATION NUMBER: US/11/109,593
; CURRENT FILING DATE: 2005-04-18
; PRIOR APPLICATION NUMBER: US 60/563,843
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 67323
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-11-109-593-1

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Best Local Similarity 89.5%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 15
US-10-322-281-691

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; Sequence 691, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc S. Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 691
; LENGTH: 155350
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(155350)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-691
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Best Local Similarity 89.5%; Pred. No. 1.8e+02;
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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 2: /SIDSS/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 4: /SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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- 15: /SIDSS/ptodata/1/pubpna/US11_NEW_PUB.seq:*
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- 19: /SIDSS/ptodata/1/pubpna/US16_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	19	100.0	977	12	US-10-301-480-570506
2	19	100.0	977	12	US-10-301-480-1183915
3	17.4	91.6	975	12	US-10-301-480-576105
4	17.4	91.6	975	12	US-10-301-480-1189514
5	15.8	83.2	36360	10	US-10-995-561-13498
6	15.4	81.1	1318	18	US-11-282-000-13
7	15	78.9	3236	18	US-11-036-196-1951
8	15	78.9	3581	17	US-11-136-527-3057
9	14.8	77.9	828	11	US-10-932-182A-80342
10	14.8	77.9	828	11	US-10-932-182A-80342
11	14.8	77.9	1455	11	US-10-932-182A-80341
12	14.8	77.9	1455	11	US-10-932-182A-80341
13	14.8	77.9	1614	18	US-11-096-568A-19074
14	14.4	75.8	3405	11	US-10-932-182A-77844

15	14.4	75.8	3405	11	US-10-932-182A-77844	Sequence 77844, A
16	14.4	75.8	162289	17	US-11-121-086-20	Sequence 20, Appl
17	14.2	74.7	21	10	US-10-310-914A-107405	Sequence 107405,
18	14.2	74.7	25	11	US-10-933-982-216667	Sequence 216667,
19	14.2	74.7	379	10	US-10-527-500-76	Sequence 76, Appl
20	14.2	74.7	497	12	US-10-301-480-467810	Sequence 467810,
21	14.2	74.7	497	12	US-10-301-480-1081219	Sequence 1081219,
22	14.2	74.7	500	7	US-09-925-065A-400591	Sequence 400591,
23	14.2	74.7	531	7	US-09-925-065A-829581	Sequence 829581,
24	14.2	74.7	532	7	US-09-925-065A-759970	Sequence 759970,
25	14.2	74.7	538	7	US-09-925-065A-822760	Sequence 822760,
26	14.2	74.7	564	7	US-09-925-065A-882339	Sequence 882339,
27	14.2	74.7	564	7	US-09-925-065A-882340	Sequence 882340,
28	14.2	74.7	574	7	US-09-925-065A-545421	Sequence 545421,
29	14.2	74.7	574	7	US-09-925-065A-545422	Sequence 545422,
30	14.2	74.7	582	7	US-09-925-065A-802642	Sequence 802642,
31	14.2	74.7	591	7	US-09-925-065A-806815	Sequence 806815,
32	14.2	74.7	592	7	US-09-925-065A-52798	Sequence 52798, A
33	14.2	74.7	592	11	US-10-301-480-154036	Sequence 154036,
34	14.2	74.7	592	12	US-10-301-480-767445	Sequence 767445,
35	14.2	74.7	597	7	US-09-925-065A-802303	Sequence 802303,
36	14.2	74.7	597	7	US-09-925-065A-802401	Sequence 802401,
37	14.2	74.7	597	7	US-09-925-065A-802539	Sequence 802539,
38	14.2	74.7	598	7	US-09-925-065A-495552	Sequence 495552,
39	14.2	74.7	600	17	US-11-136-527-6618	Sequence 6618, Ap
40	14.2	74.7	702	7	US-09-925-065A-598630	Sequence 598630,
41	14.2	74.7	702	7	US-09-925-065A-598631	Sequence 598631,
42	14.2	74.7	714	11	US-10-301-480-100859	Sequence 100859,
43	14.2	74.7	714	12	US-10-301-480-714268	Sequence 714268,
44	14.2	74.7	875	18	US-11-096-568A-10111	Sequence 10111, A
45	14.2	74.7	928	18	US-11-096-568A-18550	Sequence 18550, A

ALIGNMENTS

RESULT 1
US-10-301-480-570506
; Sequence 570506, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 570506
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-570506

Query Match 100.0%; Score 19; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCGCTGTGGCGAAGG 19
| | | | | | | | | | | | | | | | | | | | |
DB 13 GGTGCGCTGTGGCGAAGG 31

RESULT 2
US-10-301-480-1183915
; Sequence 1183915, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1183915
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1183915
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Query Match          100.0%; Score 19; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 2.1; Mismatches 0; Indels 0; Gaps 0;
Matches 19; Conservative 0;

QY 1 GGTGCGCTGTGGCGAAGG 19
   |||||
Db 13 GGTGCGCTGTGGCGAAGG 31
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RESULT 3
US-10-301-480-576105
; Sequence 576105, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 576105
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 57, 206
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-576105
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Query Match          91.6%; Score 17.4; DB 12; Length 975;
Best Local Similarity 94.7%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 GGTGCGCTGTGGCGAAGG 19
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Db 6 GGTGCGCTGTGGCGAAGG 24
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RESULT 4
US-10-301-480-1189514
; Sequence 1189514, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
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; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1189514
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 57, 206
; OTHER INFORMATION: n = A,T,C or G
US-10-301-480-1189514
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Query Match          91.6%; Score 17.4; DB 12; Length 975;
Best Local Similarity 94.7%; Pred. No. 15; Mismatches 1; Indels 0; Gaps 0;
Matches 18; Conservative 0;

QY 1 GGTGCGCTGTGGCGAAGG 19
   |||||
Db 6 GGTGCGCTGTGGCGAAGG 24
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RESULT 5
US-10-995-561-13498/c
; Sequence 13498, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13498
; LENGTH: 36360
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-13498
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Query Match          83.2%; Score 15.8; DB 10; Length 36360;
Best Local Similarity 89.5%; Pred. No. 84; Mismatches 2; Indels 0; Gaps 0;
Matches 17; Conservative 0;

QY 1 GGTGCGCTGTGGCGAAGG 19
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Db 24538 GGTGCGCTGTGGCGAAGG 24520
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RESULT 6
US-11-282-000-13
; Sequence 13, Application US/11282000
; Publication No. US20060068477A1
; GENERAL INFORMATION:
; APPLICANT: Dodge, Timothy C.
; APPLICANT: Valle, Fernando
; TITLE OF INVENTION: Methods for the Production of Products
; TITLE OF INVENTION: in Host Cells
; FILE REFERENCE: GC620-3
; CURRENT APPLICATION NUMBER: US/11/282,000
; CURRENT FILING DATE: 2005-11-17
; PRIOR APPLICATION NUMBER: US 10/116,821
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/282,277
; PRIOR FILING DATE: 2001-04-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 13
; LENGTH: 1518
; TYPE: DNA
; ORGANISM: Pantoea citrea
US-11-282-000-13

Query Match      81.1%; Score 15.4; DB 18; Length 1518;
Best Local Similarity 94.1%; Pred. No. 1.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCGCTGCTGGCGGAA 17
    ||| ||||| ||||| |||||
Db 1237 GGTGGCGCTGGCGGAA 1253

RESULT 7
US-11-036-196-1951/c
; Sequence 1951, Application US/11036196
; Publication No. US20060078900A1
; GENERAL INFORMATION:
; APPLICANT: Mendrick, Donna
; APPLICANT: Porter, Mark
; APPLICANT: Johnson, Kory
; APPLICANT: Higgin, Brandon
; APPLICANT: Castle, Arthur
; APPLICANT: Elashoff, Michael
; TITLE OF INVENTION: Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5089-US
; CURRENT APPLICATION NUMBER: US/11/036,196
; CURRENT FILING DATE: 2005-01-18
; PRIOR APPLICATION NUMBER: US/10/152,319
; PRIOR FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: US 60/292,335
; PRIOR FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/297,523
; PRIOR FILING DATE: 2001-06-13
; PRIOR APPLICATION NUMBER: US 60/298,925
; PRIOR FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: US 60/303,810
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,807
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/303,808
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/315,047
; PRIOR FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: US 60/324,928
; PRIOR FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US 60/330,867
; PRIOR FILING DATE: 2001-11-01
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1951
; LENGTH: 3236
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. NM_031814
US-11-036-196-1951

Query Match      78.9%; Score 15; DB 18; Length 3236;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGCTGGCGGAA 19
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Db 216 GCGCTGCTGGCGGAA 202

RESULT 8
US-11-136-527-3057/c
; Sequence 3057, Application US/11136527
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; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 3057
; LENGTH: 3581
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-3057

Query Match      78.9%; Score 15; DB 17; Length 3581;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GCGCTGCTGGCGGAA 19
    ||| ||||| ||||| |||||
Db 216 GCGCTGCTGGCGGAA 202

RESULT 9
US-10-932-182A-80342/c
; Sequence 80342, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patent in version 3.3
; SEQ ID NO 80342
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80342

Query Match      77.9%; Score 14.8; DB 11; Length 828;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGCGAAG 19
    ||| ||||| ||||| |||||
Db 182 GCGCGCTGTGTGTAAG 165

RESULT 10
US-10-932-182A-80342/c
; Sequence 80342, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80342
; LENGTH: 828
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80342

Query Match 77.9%; Score 14.8; DB 11; Length 828;
Best Local Similarity 88.9%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGCGAAG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 182 GCGCGCTGTGTGAAG 165

RESULT 11
US-10-932-182A-80341/c
; Sequence 80341, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80341
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80341

Query Match 77.9%; Score 14.8; DB 11; Length 1455;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGCGAAG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 182 GCGCGCTGTGTGAAG 165

RESULT 12
US-10-932-182A-80341/c
; Sequence 80341, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 80341
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-80341

Query Match 77.9%; Score 14.8; DB 11; Length 1455;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTCGCGCTGTGGCGAAG 19
| | | | | | | | | | | | | | | | | | | | | |
Db 182 GCGCGCTGTGTGAAG 165

RESULT 13
US-11-096-568A-19074
; Sequence 19074, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:

; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Therby
; FILE REFERENCE: 2750-1592FUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 19074
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Zea mays subsp. mays
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(1614)
; OTHER INFORMATION: Ceres Seq. ID no. 12368767
US-11-096-568A-19074

Query Match 77.9%; Score 14.8; DB 18; Length 1614;
Best Local Similarity 88.9%; Pred. No. 3.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTCGCGCTGTGGCGAAG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 383 GATCGCGCTGTGGCAAG 400

RESULT 14
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77844

Query Match 75.8%; Score 14.4; DB 11; Length 3405;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTCGCGCTGTGGCGA 16
| | | | | | | | | | | | | | | | | | | | | |
Db 2878 GGTCTCGCTGTGGCGA 2893

RESULT 15
US-10-932-182A-77844
; Sequence 77844, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

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; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 77844
; LENGTH: 3405
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-77844

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Query Match      75.8%; Score 14.4; DB 11; Length 3405;
Best Local Similarity 93.8%; Pred. No. 5.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      2878 GGTCTGGCTGTGGCGA 2893

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OM nucleic - nucleic search, using sw model

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Title: US-09-904-968A-20

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Maximum Match 100%
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SUMMARIES

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3	16	100.0	30	3	US-09-052-262-15
4	16	100.0	1281	3	US-09-902-540-2359
C 5	16	100.0	13941	3	US-09-799-451-341
C 6	16	100.0	14060	3	US-08-658-136-4
C 7	16	100.0	14136	3	US-10-083-246A-1
C 8	16	100.0	14148	3	US-09-052-469-7
C 9	16	100.0	14148	3	US-08-422-582-7
C 10	16	100.0	14148	3	US-09-052-262-7
C 11	16	100.0	15447	3	US-09-902-540-1100
C 12	16	100.0	31571	2	US-08-323-443B-1
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C 16	15	93.8	30	3	US-09-052-469-16
C 17	15	93.8	30	3	US-08-422-582-16
C 18	15	93.8	30	3	US-09-052-262-16
C 19	15	93.8	511	3	US-10-324-316-25
C 20	15	93.8	996	3	US-09-252-991A-2201
C 21	15	93.8	1530	3	US-09-902-540-4366
C 22	15	93.8	1641	3	US-09-252-991A-2551
C 23	15	93.8	1791	3	US-09-252-991A-2363
C 24	15	93.8	3135	3	US-09-252-991A-2282

Sequence 1216, Ap
Sequence 1395, Ap
Sequence 15903, A
Sequence 8251, Ap
Sequence 3456, Ap
Sequence 2, Appli
Sequence 2, Appli
Sequence 297, App
Sequence 301, App
Sequence 8579, Ap
Sequence 6036, Ap
Sequence 7071, Ap
Sequence 4360, Ap
Sequence 15875, A
Sequence 7887, Ap
Sequence 240, App
Sequence 4278, Ap
Sequence 3847, Ap
Sequence 1, Appli
Sequence 2837, Ap

25 15 93.8 23694 3 US-09-902-540-1216
26 14.4 90.0 354 3 US-09-489-039A-1395
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28 14.4 90.0 435 3 US-09-902-540-8251
C 29 14.4 90.0 594 3 US-09-902-540-3456
C 30 14.4 90.0 688 2 US-08-840-683-2
C 31 14.4 90.0 688 2 US-08-555-722-2
C 32 14.4 90.0 688 3 US-09-384-301-2
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C 39 14.4 90.0 981 3 US-09-252-991A-15875
C 40 14.4 90.0 1032 3 US-09-252-991A-7887
C 41 14.4 90.0 1542 3 US-09-902-540-240
C 42 14.4 90.0 1785 3 US-09-252-991A-4278
C 43 14.4 90.0 1899 3 US-09-902-540-3847
C 44 14.4 90.0 2219 2 US-08-606-322-1
C 45 14.4 90.0 2289 3 US-09-489-039A-2837

ALIGNMENTS

RESULT 1
US-09-052-469-15
; Sequence 15, Application US/09052469
; Patent No. 6380360
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE.1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,469
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-09-052-469-15

Query Match 100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
Db 5 CGCGCGGCGGCATCGT 20

RESULT 2
US-08-422-582-15
; Sequence 15, Application US/08422582
; Patent No. 6485960
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: 75 State Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/422,582
; FILING DATE: 14-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/53313 (MRC-006xx)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
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; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-08-422-582-15

Query Match 100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
Db 5 CGCGCGGCGGCATCGT 20

RESULT 3
US-09-052-262-15
; Sequence 15, Application US/09052262
; Patent No. 6656681
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,262
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9326470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cdna
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
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; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-09-052-262-15

Query Match      100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
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Db 5 CGCGCGGCGGCATCGT 20
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RESULT 4
US-09-902-540-2359
; Sequence 2359, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2359
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2359

Query Match      100.0%; Score 16; DB 3; Length 1281;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
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Db 257 CGCGCGGCGGCATCGT 272
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RESULT 5
US-09-799-451-341/c
; Sequence 341, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05

; NAME/KEY: misc_feature
; LOCATION: 1..30
; OTHER INFORMATION: /function= "N2765 primer"
US-09-052-262-15

Query Match      100.0%; Score 16; DB 3; Length 30;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
   |||||
Db 5 CGCGCGGCGGCATCGT 20
   |||||

RESULT 4
US-09-902-540-2359
; Sequence 2359, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 2359
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-2359

Query Match      100.0%; Score 16; DB 3; Length 1281;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
   |||||
Db 257 CGCGCGGCGGCATCGT 272
   |||||

RESULT 5
US-09-799-451-341/c
; Sequence 341, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yungqing
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/799,451
; CURRENT FILING DATE: 2001-03-05

; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 141_
; LENGTH: 13941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1547)..(13120)
US-09-799-451-341

Query Match      100.0%; Score 16; DB 3; Length 13941;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
   |||||
Db 224 CGCGCGGCGGCATCGT 209
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RESULT 6
US-08-658-136-4/c
; Sequence 4, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14060 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135..13040
US-08-658-136-4

Query Match      100.0%; Score 16; DB 3; Length 14060;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCGGGCGGCATCGT 16
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Db 147 CGCGGGCGGCATCGT 132

RESULT 7
US-10-083-246A-1/c
; Sequence 1, Application US/10083246A
; Patent No. 6916619
; GENERAL INFORMATION:
; APPLICANT: Athena Diagnostics
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 1133/2002
; CURRENT APPLICATION NUMBER: US/10/083,246A
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 168
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-083-246A-1

Query Match 100.0%; Score 16; DB 3; Length 14136;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGGGCGGCATCGT 16
    |||||
Db 224 CGCGGGCGGCATCGT 209

RESULT 8
US-09-052-469-7/c
; Sequence 7, Application US/09052469
; Patent No. 6380360
; GENERAL INFORMATION:
; APPLICANT: Harris et al.
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff, Ltd.
; STREET: One Financial Center
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk, 3.50 inch
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/052,469
; FILING DATE: Concurrently herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/422,582
; FILING DATE: 14-April-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9507766.5
; FILING DATE: 13-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411900.5
; FILING DATE: 14-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB PCT/GB94/02822
; FILING DATE: 23-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 93266470.3
; FILING DATE: 24-DEC-1993
; ATTORNEY/AGENT INFORMATION:

; NAME: Williams, Ph.D., Kathleen M.
; REGISTRATION NUMBER: 34,380
; REFERENCE/DOCKET NUMBER: 3265/74165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 345-9100
; TELEFAX: (617) 345-9111
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14148 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 212..13117
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 212..278
; OTHER INFORMATION: /note= "Probable signal sequence"
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 359..4574
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: sites at the following positions: 359, 476, 557, 572,
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 4574..8144
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: sites at following locations: 4559, 4574, 4631, 4763,
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 8363..11741
; OTHER INFORMATION: /note= "N-linked glycosylation
; OTHER INFORMATION: sites at following locations: 8471, 8663, 8732, 8843,
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 7949..8009
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; LOCATION: 8288..8348
; OTHER INFORMATION: /note= "Predicted transmembrane
; OTHER INFORMATION: domain"
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; LOCATION: 9434..9494
; OTHER INFORMATION: /note= "Predicted transmembrane
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; OTHER INFORMATION: domain"
; FEATURE:
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/ OTHER INFORMATION: /note= "Predicted transmembrane
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/ NAME/KEY: misc_feature
/ LOCATION: 11894..11954
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/ OTHER INFORMATION: domain"
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/ OTHER INFORMATION: domain"
/ FEATURE:
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/ LOCATION: 12377..12437
/ OTHER INFORMATION: /note= "Predicted transmembrane
/ OTHER INFORMATION: domain"
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/ NAME/KEY: misc_feature
/ LOCATION: 212..278
/ OTHER INFORMATION: /note= "Possible hinge sequence"
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 279
/ OTHER INFORMATION: /note= "Cleavage site"
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US-09-052-469-7

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Query Match 100.0%; Score 16; DB 3; Length 14148;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CGCGCGCGGCATCGT 16
Db 224 CGCGCGCGGCATCGT 209

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RESULT 9
US-08-422-582-7/c
/ Sequence 7, Application US/08422582
/ Patent No. 6485960
/ GENERAL INFORMATION:
/ APPLICANT: Harris et al.
/ TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE 1 GENE
/ TITLE OF INVENTION: AND USES THEREOF
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Banner & Witcoff, Ltd.
/ STREET: 75 State Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk, 3.50 inch
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Wordperfect 6.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/422,582
/ FILING DATE: 14-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9411900.5
/ FILING DATE: 14-JUN-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB PCT/GB94/02822
/ FILING DATE: 23-DEC-1994
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9507766.5
/ FILING DATE: 13-APR-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: GB 9326470.3
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/ FILING DATE: 24-DEC-1993
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Williams, Ph.D., Kathleen M.
/ REGISTRATION NUMBER: 34,380
/ REFERENCE/DOCKET NUMBER: 3265/53313 (MRC-006xx)
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 345-9100
/ TELEFAX: (617) 345-9111
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14148 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: cdna
/ ORIGINAL SOURCE:
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 212..13117
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/ NAME/KEY: misc_feature
/ LOCATION: 212..278
/ OTHER INFORMATION: /note= "Probable signal sequence"
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/ OTHER INFORMATION: sites at the following positions: 359, 476, 557, 572,
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/ OTHER INFORMATION: /note= "N-linked glycosylation
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/ LOCATION: 8363..11741
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/ OTHER INFORMATION: sites at following locations: 8471, 8663, 8732, 8843,
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 7949..8009
/ OTHER INFORMATION: /note= "Predicted transmembrane
/ OTHER INFORMATION: domain"
/ FEATURE:
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/ LOCATION: 8288..8348
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/ NAME/KEY: misc_feature
/ LOCATION: 9434..9494
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/ NAME/KEY: misc_feature
/ LOCATION: 10052..10112
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/ LOCATION: 10178..10238
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/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 10955..11015
/ OTHER INFORMATION: /note= "Predicted transmembrane

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OTHER INFORMATION: domain"
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LOCATION: 11894..11954
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FEATURE:
NAME/KEY: misc_feature
LOCATION: 12293..12353
OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 12377..12437
OTHER INFORMATION: /note= "Predicted transmembrane"
OTHER INFORMATION: domain"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 212..278
OTHER INFORMATION: /note= "Possible hinge sequence"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 279
OTHER INFORMATION: /note= "Cleavage site"
US-09-052-262-7

Query Match 100.0%; Score 16; DB 3; Length 14148;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
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DB 224 CGCGCGGCGGCATCGT 209

RESULT 11
US-09-902-540-1100/c
Sequence 1100, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 1100
LENGTH: 15447
TYPE: DNA
ORGANISM: Myxococcus xanthus
US-09-902-540-1100
Query Match 100.0%; Score 16; DB 3; Length 15447;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGCGGCGGCATCGT 16
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DB 3663 CGCGCGGCGGCATCGT 3648

RESULT 12
US-08-323-443B-1
Sequence 1, Application US/08323443B
Patent No. 5654170
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: DACKOWSKI, WILLIAM R.
APPLICANT: GERMINO, GREGORY
APPLICANT: QIAN, FENG
TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby PC
STREET: 805 Third Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,443B
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, S. Peter
REGISTRATION NUMBER: 25,351
REFERENCE/DOCKET NUMBER: 0372/OA462
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 31571 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: PKD1 GENOMIC
US-08-323-443B-1

Query Match 100.0%; Score 16; DB 2; Length 31571;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 3273 CGCGCGGCGGCATCGT 3288

RESULT 13
US-08-658-136-2/c
Sequence 2, Application US/08658136
Patent No. 6071717
GENERAL INFORMATION:
APPLICANT: KLINGER, KATHERINE W.
APPLICANT: LANDES, GREGORY M.
APPLICANT: BURN, TIMOTHY C.
APPLICANT: CONNORS, TIMOTHY D.
APPLICANT: DACKOWSKI, WILLIAM

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; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
;
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53526 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-2
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; Query Match 100.0%; Score 16; DB 3; Length 53526;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CGCGCGGCGGCATCGT 16
; Db 3660 CGCGCGGCGGCATCGT 3645
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; RESULT 14
; US-08-658-136-1/c
; Sequence 1, Application US/08658136
; Patent No. 6071717
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
;
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,136
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; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: LASSEN, ELIZABETH
; REGISTRATION NUMBER: 31,845
; REFERENCE/DOCKET NUMBER: GEN4-17.8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; MOLECULE TYPE: DNA (genomic)
; US-08-658-136-1
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; Query Match 100.0%; Score 16; DB 3; Length 53577;
; Best Local Similarity 100.0%; Pred. No. 1.2e+02;
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 CGCGCGGCGGCATCGT 16
; Db 3660 CGCGCGGCGGCATCGT 3645
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; RESULT 15
; US-08-460-215A-1/c
; Sequence 1, Application US/08460215A
; Patent No. 6867288
; GENERAL INFORMATION:
; APPLICANT: KLINGER, KATHERINE W
; APPLICANT: LANDES, GREGORY M
; APPLICANT: BURN, TIMOTHY C
; APPLICANT: CONNORS, TIMOTHY D
; APPLICANT: DACKOWSKI, WILLIAM
; APPLICANT: GERMINO, GREGORY
; APPLICANT: QIAN, FENG
; TITLE OF INVENTION: POLYCYSTIC KIDNEY DISEASE GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENZYME CORPORATION
; STREET: ONE MOUNTAIN ROAD
; CITY: FRAMINGHAM
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 01701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,215A
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DUGAN, DEBORAH
; REGISTRATION NUMBER: 37,315
; REFERENCE/DOCKET NUMBER: GEN4-17.5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 508-872-8400
; TELEFAX: 508-872-5415
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 53577 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-460-215A-1
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Query Match 100.0%; Score 16; DB 3; Length 53577;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCGGGGGCGCATCGT 16
 Db 3660 CGCGGGGGCGCATCGT 3645

Search completed: May 9, 2006, 05:56:08
 Job time : 45.0889 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:26:49 ; Search time 387.378 Seconds
(without alignments)
341.553 Million cell updates/sec

Title: US-09-904-968A-20

Perfect score: 16

Sequence: 1 cggcgggcgccatcgt 16

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Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	16	100.0	16	3	US-09-904-968A-20
2	16	100.0	485	5	US-10-027-632-292667
3	16	100.0	485	6	US-10-027-632-292667
4	16	100.0	619	7	US-10-767-701-4510
5	16	100.0	4052	6	US-10-156-761-875
6	16	100.0	12992	6	US-10-080-334-89
7	16	100.0	13941	7	US-10-302-172-341
8	16	100.0	14136	3	US-09-964-824A-244
9	16	100.0	14136	6	US-10-083-246A-1
10	16	100.0	14136	9	US-10-843-641A-5547
11	16	100.0	14136	9	US-10-411-915-1
12	16	100.0	14136	9	US-10-956-157-385
13	16	100.0	14169	9	US-10-450-763-17056
14	16	100.0	53522	3	US-09-904-968A-1
15	16	100.0	9025608	6	US-10-156-761-1
16	15	93.8	25	8	US-10-719-900-515844
17	15	93.8	261	8	US-10-425-115-80381
18	15	93.8	486	7	US-10-437-963-45611
19	15	93.8	511	6	US-10-324-316-25
20	15	93.8	511	10	US-11-038-329-25
21	15	93.8	540	7	US-10-282-122A-33759
22	15	93.8	615	7	US-10-437-963-36162
23	15	93.8	687	7	US-10-437-963-34646

24	15	93.8	738	8	US-10-425-115-34043	Sequence 34043, A
25	15	93.8	793	7	US-10-425-114-27555	Sequence 27555, A
26	15	93.8	819	6	US-10-369-493-32278	Sequence 32278, A
27	15	93.8	822	8	US-10-425-115-136862	Sequence 136862, A
28	15	93.8	897	6	US-10-369-493-28520	Sequence 28520, A
29	15	93.8	897	6	US-10-369-493-31279	Sequence 31279, A
30	15	93.8	905	8	US-10-425-115-148261	Sequence 148261, A
31	15	93.8	1020	9	US-10-494-495-2	Sequence 2, Appli
32	15	93.8	1032	6	US-10-156-761-3524	Sequence 3524, Ap
33	15	93.8	1269	6	US-10-369-493-31563	Sequence 13563, A
34	15	93.8	1355	7	US-10-767-701-13547	Sequence 13547, A
35	15	93.8	1389	7	US-10-425-114-4125	Sequence 4125, Ap
36	15	93.8	1448	7	US-10-425-114-23975	Sequence 23975, A
37	15	93.8	1704	7	US-10-282-122A-13582	Sequence 13582, A
38	15	93.8	1704	7	US-10-282-122A-14054	Sequence 14054, A
39	15	93.8	1721	8	US-10-425-115-55704	Sequence 55704, A
40	15	93.8	1875	7	US-10-437-963-36156	Sequence 36156, A
41	15	93.8	4786	7	US-10-437-963-18794	Sequence 18794, A
42	15	93.8	29870	9	US-10-915-740A-12	Sequence 12, Appli
43	15	93.8	102634	9	US-10-915-740A-12	Sequence 12, Appli
44	15	93.8	135638	6	US-10-314-657-1	Sequence 1, Appli
45	15	93.8	135638	9	US-10-473-193-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-904-968A-20

; Sequence 20, Application US/09904968A

; Publication No. US20030008288A1

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

; APPLICANT: GERMINO, Gregory

; APPLICANT: WATNICK, Terry

; APPLICANT: PHAKDEEKITCHAROEN, Bunyong

; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE

; FILE REFERENCE: JHU1680-2

; CURRENT APPLICATION NUMBER: US/09/904,968A

; CURRENT FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/283,691

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/218,261

; PRIOR FILING DATE: 2000-07-13

; NUMBER OF SEQ ID NOS: 113

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 20

; LENGTH: 16

; TYPE: DNA

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: PCR primer 1R1

US-09-904-968A-20

Query Match 100.0%; Score 16; DB 3; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16

DB 1 CGCGCGGCGGCATCGT 16

RESULT 2

US-10-027-632-292667/c

; Sequence 292667, Application US/10027632

; Publication No. US20020198371A1

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

; TITLE OF INVENTION: Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027,632

; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292667
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Human
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS81577_1
US-10-027-632-292667

Query Match 100.0%; Score 16; DB 5; Length 485;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
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Db 20 CGCGCGGCGGCATCGT 5

RESULT 3

US-10-027-632-292667/c
; Sequence 292667, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 292667
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-292667

Query Match 100.0%; Score 16; DB 6; Length 485;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
|||
Db 20 CGCGCGGCGGCATCGT 5

RESULT 4

US-10-767-701-4510
; Sequence 4510, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yihwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 4510
; LENGTH: 619
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS81577_1
US-10-767-701-4510

Query Match 100.0%; Score 16; DB 7; Length 619;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
|||
Db 253 CGCGCGGCGGCATCGT 268

RESULT 5

US-10-156-761-875
; Sequence 875, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 875
; LENGTH: 4062
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (4062)
US-10-156-761-875

Query Match 100.0%; Score 16; DB 6; Length 4062;
Best Local Similarity 100.0%; Pred. No. 55;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
|||
Db 2966 CGCGCGGCGGCATCGT 2981

RESULT 6

US-10-080-334-89/c

; Sequence 89, Application US/10080334
; Publication No. US20040002584A1
; GENERAL INFORMATION:
; APPLICANT: Pena, Carol E. A.
; APPLICANT: Shimkets, Richard A
; APPLICANT: Li, Li
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Vernet, Corine A. M.
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Guo, Xiaojia
; APPLICANT: Gusev, Vladimir Y
; APPLICANT: Casman, Stacie J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Furtak, Katarzyna
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Patturajan, Meera
; APPLICANT: Gangolli, Bsha A
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Liu, Xiaohong
; APPLICANT: Baumgartner, Jason C.
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spaderna, Steven K
; APPLICANT: Zerhusen, Bryan D
; TITLE OF INVENTION: Proteins, Polynucleotides Encoding Them and Methods of
; FILE REFERENCE: 21402-275
; CURRENT APPLICATION NUMBER: US/10/080,334
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/270,523
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/322,712
; PRIOR FILING DATE: 2001-09-17
; PRIOR APPLICATION NUMBER: 60/311,980
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/330,307
; PRIOR FILING DATE: 2001-10-18
; PRIOR APPLICATION NUMBER: 60/278,796
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/281,521
; PRIOR FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: 60/276,677
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/311,595
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: 60/270,220
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: 60/274,295
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/318,526
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/286,548
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 60/291,765
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/270,797
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/276,400
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/270,810
; PRIOR FILING DATE: 2001-02-23
; NUMBER OF SEQ ID NOS: 398
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 89
; LENGTH: 12992
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-080-334-89

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Best Local Similarity 100.0%; Pred. No. 44;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
Db 65 CGCGCGGCGGCATCGT 50
RESULT 7
US-10-302-172-341/c
; Sequence 341, Application US/10302172
; Publication No. US20040053250A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. US20040053250A1 Arginine-rich Protein-like Nucleic Acids
; FILE REFERENCE: 803_1CNCP
; CURRENT APPLICATION NUMBER: US/10/302,172
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/225,251
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: PCT US02/05095
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 09/799,451
; PRIOR FILING DATE: 2001-03-05
; NUMBER OF SEQ ID NOS: 950
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 341
; LENGTH: 13941
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1547)..(13120)
US-10-302-172-341

Query Match 100.0%; Score 16; DB 7; Length 13941;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
Db 224 CGCGCGGCGGCATCGT 209

RESULT 8
US-09-964-824A-244/c
; Sequence 244, Application US/09964824A
; Patent No. US20020102531A1
; GENERAL INFORMATION:
; APPLICANT: Horrigan, Stephen
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signatu
; FILE REFERENCE: 689290-73
; CURRENT APPLICATION NUMBER: US/09/964,824A
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: US/60/236,033
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,032
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US/60/236,028
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 583
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 244
; LENGTH: 14136
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-824A-244

Query Match 100.0%; Score 16; DB 3; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 9

US-10-083-246A-1/c

; Sequence 1, Application US/10083246A

; Publication No. US20030152936A1

; GENERAL INFORMATION:

; APPLICANT: Athena Diagnostics

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY

; TITLE OF INVENTION: DISEASE

; FILE REFERENCE: 1133/2002

; CURRENT APPLICATION NUMBER: US/10/083,246A

; CURRENT FILING DATE: 2002-10-15

; NUMBER OF SEQ ID NOS: 168

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 14136

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-083-246A-1

Query Match 100.0%; Score 16; DB 6; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 10

US-10-843-641A-5547/c

; Sequence 5547, Application US/10843641A

; Publication No. US20050064454A1

; GENERAL INFORMATION:

; APPLICANT: Avalon Pharmaceuticals, Inc.

; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using

; TITLE OF INVENTION: Signature Gene Sets

; FILE REFERENCE: 689290-189

; CURRENT APPLICATION NUMBER: US/10/843,641A

; CURRENT FILING DATE: 2004-05-12

; PRIOR APPLICATION NUMBER: US/09/873,367

; PRIOR FILING DATE: 2001-06-05

; PRIOR APPLICATION NUMBER: US/09/954,531

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: US/09/954,456

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,436

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/962,832

; PRIOR FILING DATE: 2001-09-25

; PRIOR APPLICATION NUMBER: US/09/964,824

; PRIOR FILING DATE: 2001-09-27

; PRIOR APPLICATION NUMBER: US/09/967,768

; PRIOR FILING DATE: 2001-09-28

; PRIOR APPLICATION NUMBER: US/09/968,007

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,347

; PRIOR FILING DATE: 2001-10-02

; PRIOR APPLICATION NUMBER: US/09/969,708

; PRIOR FILING DATE: 2001-10-03

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 8447

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 5547

; LENGTH: 14136

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-843-641A-5547

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 11

US-10-411-915-1/c

; Sequence 1, Application US/10411915

; Publication No. US20050100898A1

; GENERAL INFORMATION:

; APPLICANT: Athena Diagnostics

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR GENETIC ANALYSIS OF POLYCYSTIC KIDNEY

; TITLE OF INVENTION: DISEASE

; FILE REFERENCE: 1133/2005

; CURRENT APPLICATION NUMBER: US/10/411,915

; CURRENT FILING DATE: 2003-04-11

; PRIOR APPLICATION NUMBER: US 10/083,246

; PRIOR FILING DATE: 2002-02-26

; PRIOR APPLICATION NUMBER: US 60/328,739

; PRIOR FILING DATE: 2001-10-12

; NUMBER OF SEQ ID NOS: 172

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 1

; LENGTH: 14136

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-411-915-1

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 12

US-10-956-157-385/c

; Sequence 385, Application US/10956157

; Publication No. US20050118625A1

; GENERAL INFORMATION:

; APPLICANT: Wyeth

; APPLICANT: Mounts, William

; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH

; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES

; FILE REFERENCE: 031896-043000 (AM 101081)

; CURRENT APPLICATION NUMBER: US/10/956,157

; CURRENT FILING DATE: 2004-10-04

; NUMBER OF SEQ ID NOS: 319805

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 385

; LENGTH: 14136

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-956-157-385

Query Match 100.0%; Score 16; DB 9; Length 14136;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 13

US-10-450-763-17056/c

; Sequence 17056, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 17056
; LENGTH: 14169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (212)-(9934)
; OTHER INFORMATION: 99% homologous to Homo sapiens Polycystic kidney disease 1
; OTHER INFORMATION: (PKD1) polypeptide, accession number W00870, Smith-Waterman Score=
US-10-450-763-17056

Query Match 100.0%; Score 16; DB 9; Length 14169;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGGCGGCATCGT 16
Db 224 CGGCGGGCGGCATCGT 209

RESULT 14
US-09-904-968A-1/c
; Sequence 1, Application US/09904968A
; Publication No. US20030008288A1
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: GERMINO, Gregory
; APPLICANT: WATNICK, Terry
; APPLICANT: PHAKDEEKITCHAROEN, Bunyong
; TITLE OF INVENTION: DETECTION AND TREATMENT OF POLYCYSTIC KIDNEY DISEASE
; FILE REFERENCE: JHU1680-2
; CURRENT APPLICATION NUMBER: US/09/904,968A
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/283,691
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/218,261
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 53522
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-904-968A-1

Query Match 100.0%; Score 16; DB 3; Length 53522;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGGCGGGCGGCATCGT 16
Db 3660 CGGCGGGCGGCATCGT 3645

RESULT 15
US-10-156-761-1

; Sequence 1, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 1
; LENGTH: 9025608
; TYPE: DNA
; ORGANISM: Streptomyces avermitilis
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4187715)
; OTHER INFORMATION: a, t, c, g, other or unknown
US-10-156-761-1
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Best Local Similarity 100.0%; Pred. No. 13;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1064086 CGGCGGGCGGCATCGT 1064101
Search completed: May 9, 2006, 06:18:41
Job time : 398.378 secs

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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 05:37:24 ; Search time 361.956 Seconds
(without alignments)
180.024 Million cell updates/sec

Title: US-09-904-968A-20

Perfect score: 16

Sequence: 1 cggcggcgccatcgt 16

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Gapop 10.0 , Gapext 1.0

Searched: 9306428 seqs, 2036268586 residues

Total number of hits satisfying chosen parameters: 18612856

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA_New.*
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3: /SIDSS/ptodata/1/pubpna/US07_NEW_PUB.seq.*
4: /SIDSS/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16	100.0	977	12	US-10-301-480-570506
C 2	16	100.0	977	12	US-10-301-480-1183915
C 3	15	93.8	1424	18	US-11-096-568A-10796
C 4	15	93.8	1737	18	US-10-858-730-174
C 5	15	93.8	14055	13	US-10-496-351-1
C 6	15	93.8	82746	13	US-10-496-351-56
C 7	14.4	90.0	348	10	US-10-432-483-2
C 8	14.4	90.0	669	10	US-10-467-657-3407
C 9	14.4	90.0	687	10	US-10-467-657-5755
C 10	14.4	90.0	783	10	US-10-467-657-4281
C 11	14.4	90.0	852	10	US-10-467-657-2873
C 12	14.4	90.0	882	10	US-10-467-657-2875
C 13	14.4	90.0	991	10	US-10-750-185-63870
C 14	14.4	90.0	991	10	US-10-750-623-63870

15	14.4	90.0	1899	10	US-10-467-657-3439	Sequence 3439, Ap
16	14.4	90.0	1899	10	US-10-467-657-4631	Sequence 4631, Ap
C 17	14.4	90.0	2321	18	US-11-232-440-35	Sequence 36, Appl
18	14.4	90.0	8651	10	US-10-432-483-48	Sequence 48, Appl
C 19	14.4	90.0	1694969	13	US-10-506-454-1690	Sequence 1690, Ap
20	14	87.5	1593	18	US-11-079-463-4797	Sequence 4797, Ap
C 21	14	87.5	1930	18	US-11-144-947-172	Sequence 172, App
22	14	87.5	2442	13	US-10-469-469-276	Sequence 276, App
C 23	14	87.5	2683	18	US-11-144-947-301	Sequence 301, App
24	13.4	83.8	24	10	US-10-310-914A-169492	Sequence 169492, Ap
25	13.4	83.8	255	10	US-10-909-125-1990	Sequence 1990, Ap
26	13.4	83.8	389	7	US-09-925-065A-502219	Sequence 502219, Ap
C 27	13.4	83.8	396	18	US-11-250-759-167	Sequence 167, App
28	13.4	83.8	434	7	US-09-925-065A-480598	Sequence 480598, Ap
C 29	13.4	83.8	434	7	US-09-925-065A-480599	Sequence 480599, Ap
30	13.4	83.8	435	10	US-10-467-657-709	Sequence 709, App
C 31	13.4	83.8	447	10	US-10-467-657-711	Sequence 711, App
32	13.4	83.8	471	7	US-09-925-065A-386550	Sequence 386550, Ap
33	13.4	83.8	471	7	US-09-925-065A-386551	Sequence 386551, Ap
34	13.4	83.8	471	7	US-09-925-065A-386552	Sequence 386552, Ap
35	13.4	83.8	476	12	US-10-301-480-455124	Sequence 455124, Ap
36	13.4	83.8	476	12	US-10-301-480-455125	Sequence 455125, Ap
37	13.4	83.8	476	12	US-10-301-480-455126	Sequence 455126, Ap
38	13.4	83.8	476	12	US-10-301-480-1068533	Sequence 1068533, Ap
39	13.4	83.8	476	12	US-10-301-480-1068534	Sequence 1068534, Ap
40	13.4	83.8	476	12	US-10-301-480-1068535	Sequence 1068535, Ap
C 41	13.4	83.8	512	17	US-11-181-587-21	Sequence 21, Appl
C 42	13.4	83.8	651	17	US-11-143-401-13	Sequence 13, Appl
C 43	13.4	83.8	654	17	US-11-052-554A-710	Sequence 710, Appl
44	13.4	83.8	680	12	US-10-301-480-536297	Sequence 536297, Ap
45	13.4	83.8	680	12	US-10-301-480-1149706	Sequence 1149706, Ap

ALIGNMENTS

RESULT 1
US-10-301-480-570506/c
; Sequence 570506, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 10827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1228818
; SOFTWARE: FASTSQ For Windows Version 4.0
; SEQ ID NO 570506
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-570506

Query Match 100.0%; Score 16; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCGCGCGCGCATCGT 16
DB 339 CGCGCGCGCGCATCGT 324

RESULT 2
US-10-301-480-1183915/c
; Sequence 1183915, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1183915
; LENGTH: 977
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480-1183915

Query Match 100.0%; Score 16; DB 12; Length 977;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCGT 16
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Db 339 CGCGCGGCGGCATCGT 324

RESULT 3
US-11-096-568A-10796
; Sequence 10796, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nikolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096,568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 10796
; LENGTH: 1424
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(1424)
; OTHER INFORMATION: Ceres Seq. ID no. 13597194
US-11-096-568A-10796

Query Match 93.8%; Score 15; DB 18; Length 1424;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCG 15
| | | | | | | | | | | | | |
Db 240 CGCGCGGCGGCATCG 254

RESULT 4
US-10-858-730-174/c
; Sequence 174, Application US/10858730
; Publication No. US20050255568A1
; GENERAL INFORMATION:
; APPLICANT: Bailey, Richard B.
; APPLICANT: Blomquist, Paul
; APPLICANT: Doten, Reed
; APPLICANT: Driggers, Edward M.
; APPLICANT: Madden, Kevin T.
; APPLICANT: O'Leary, Jessica
; APPLICANT: O'Toole, George
; APPLICANT: Trueheart, Joshua
; APPLICANT: Walbridge, Michael J.
; APPLICANT: Yorgey, Peter S.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR AMINO ACID
; TITLE OF INVENTION: PRODUCTION
; FILE REFERENCE: 14184-030001
; CURRENT APPLICATION NUMBER: US/10/858,730
; CURRENT FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/475,000
; PRIOR FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US 60/551,860
; PRIOR FILING DATE: 2004-03-10
; NUMBER OF SEQ ID NOS: 364
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 1737
; TYPE: DNA
; ORGANISM: Streptomyces coelicolor
US-10-858-730-174

Query Match 93.8%; Score 15; DB 10; Length 1737;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCG 15
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Db 991 CGCGCGGCGGCATCG 977

RESULT 5
US-10-496-351-1/c
; Sequence 1, Application US/10496351
; Publication No. US20060084141A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 14055
; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-1

Query Match 93.8%; Score 15; DB 13; Length 14055;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGCGGCGGCATCG 15
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Db 13723 CGCGCGGCGGCATCG 13709

RESULT 6
US-10-496-351-56
; Sequence 56, Application US/10496351
; Publication No. US20060084141A1
; GENERAL INFORMATION:
; APPLICANT: Floss, Heinz
; APPLICANT: Yu, Tin-Wein
; APPLICANT: Leistner, Eckard
; TITLE OF INVENTION: Biosynthetic Gene Cluster for the Maytansinoid Antitumor Agent
; FILE REFERENCE: UWASH-06712
; CURRENT APPLICATION NUMBER: US/10/496,351
; CURRENT FILING DATE: 2004-05-19
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 82746

; TYPE: DNA
; ORGANISM: Actinosynnema pretiosum
US-10-496-351-56

Query Match 93.8%; Score 15; DB 13; Length 82746;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCG 15
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Db 23319 CGGCGGGCGGCATCG 23333

RESULT 7
US-10-432-483-2
; Sequence 2, Application US/10432483
; Publication No. US20050260699A1
; GENERAL INFORMATION:
; APPLICANT: deSouza, Mervyn L.
; APPLICANT: Jessen, Holly
; APPLICANT: Schroeder, William A.
; APPLICANT: Gokarn, Ravi R.
; TITLE OF INVENTION: CAROTENOID BIOSYNTHESIS
; FILE REFERENCE: 12799-002081
; CURRENT APPLICATION NUMBER: US/10/432,483
; CURRENT FILING DATE: 2003-11-10
; PRIOR APPLICATION NUMBER: PCT/US01/43906
; PRIOR FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: US 60/252,749
; PRIOR FILING DATE: 2000-11-22
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 348
; TYPE: DNA
; ORGANISM: Agromyces mediolanus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(345)
US-10-432-483-2

Query Match 90.0%; Score 14.4; DB 10; Length 348;
Best Local Similarity 93.8%; Pred. No. 1.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
|||||
Db 107 CGGCGGGCGGCCTCGT 122

RESULT 8
US-10-467-657-3407/c
; Sequence 3407, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 3407
; LENGTH: 669
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3407

Query Match 90.0%; Score 14.4; DB 10; Length 669;
Best Local Similarity 93.8%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
|||||
Db 104 CGGCGGGCGGCATCGT 89

RESULT 9
US-10-467-657-5755/c
; Sequence 5755, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 5755
; LENGTH: 687
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-5755

Query Match 90.0%; Score 14.4; DB 10; Length 687;
Best Local Similarity 93.8%; Pred. No. 99;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
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Db 338 CAGCGGGCGGCATCGT 323

RESULT 10
US-10-467-657-4281
; Sequence 4281, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 4281
; LENGTH: 783
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-4281

Query Match 90.0%; Score 14.4; DB 10; Length 783;
Best Local Similarity 93.8%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGGCGGGCGGCATCGT 16
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Db 566 CGCGGCGGCATCGT 581

RESULT 11

US-10-467-657-2873
; Sequence 2873, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2873
; LENGTH: 852
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2873

Query Match 90.0%; Score 14.4; DB 10; Length 852;
Best Local Similarity 93.8%; Pred. No. 94;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGGCATCGT 16

|||||

Db 744 CGCGGGCGGCATCGT 759

RESULT 12

US-10-467-657-2875/c
; Sequence 2875, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04
; SEQ ID NO 2875
; LENGTH: 882
; TYPE: DNA
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-2875

Query Match 90.0%; Score 14.4; DB 10; Length 882;
Best Local Similarity 93.8%; Pred. No. 93;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGGCATCGT 16

|||||

Db 121 CGCGGGCGGCATCGT 106

RESULT 13

US-10-750-185-63870/c
; Sequence 63870, Application US/10750185
; Publication No. US20050260603A1

; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63870
; LENGTH: 991
; TYPE: DNA
; ORGANISM: Bovine 19866881191767
US-10-750-185-63870

Query Match 90.0%; Score 14.4; DB 10; Length 991;
Best Local Similarity 93.8%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGGCATCGT 16

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Db 450 CGCGAGCGGCATCGT 435

RESULT 14

US-10-750-623-63870/c
; Sequence 63870, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63870
; LENGTH: 991
; TYPE: DNA
; ORGANISM: Bovine 19866881191767
US-10-750-623-63870

Query Match 90.0%; Score 14.4; DB 10; Length 991;
Best Local Similarity 93.8%; Pred. No. 90;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCGGGCGGCATCGT 16

|||||

Db 450 CGCGAGCGGCATCGT 435

RESULT 15

US-10-467-657-3439
; Sequence 3439, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita

APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 3439
LENGTH: 1899
TYPE: DNA
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-3439

Query Match 90.0%; Score 14.4; DB 10; Length 1899;
Best Local Similarity 93.8%; Pred. No. 78;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CGGCGGCGGCATCGT 16
Db 656 CGGCGGCGGCATCGT 671

Search completed: May 9, 2006, 06:39:10
Job time : 361.956 secs

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axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19
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Db 11 TGGCCCTTCC 1

RESULT 3
AJ734312/c
LOCUS
DEFINITION      10 bp mRNA linear EST 17-FEB-2005
ACCESSION      AJ734312
VERSION        AJ734312.1 GI:53899699
KEYWORDS       EST
SOURCE         Gallus gallus (chicken)
ORGANISM       Gallus gallus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                Phasianinae; Gallus.
REFERENCE
AUTHORS         Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezubov,Y., Zaim,J.,
                Fiedler,P., Kutter,S., Biagodatski,A., Kostovska,D., Koter,M.,
                Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
TITLE           Full-length cDNAs from chicken bursal lymphocytes to facilitate
                gene function analysis
JOURNAL         Genome Biol. 6 (1), R6 (2005)
PUBMED         15642098
COMMENT         Contact: Caldwell RB
                GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
                Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.

FEATURES
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Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ACTCAT 9
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Db 10 ACTCAT 4

RESULT 4
CA795700
LOCUS
DEFINITION      10 bp mRNA linear EST 05-DEC-2002
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ACCESSION      CA795700
VERSION        CA795700.1 GI:26052776
KEYWORDS       EST.
SOURCE         Theobroma cacao (cacao)
ORGANISM       Theobroma cacao
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axillary buds of stem explants, petioles, germinating
eyes, tubers, or roots."

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 1.5;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19
    | |||||
Db 11 TGGCCCTTCC 1

RESULT 3
AJ734312/c
LOCUS
DEFINITION      10 bp mRNA linear EST 17-FEB-2005
ACCESSION      AJ734312
VERSION        AJ734312.1 GI:53899699
KEYWORDS       EST
SOURCE         Gallus gallus (chicken)
ORGANISM       Gallus gallus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                Phasianinae; Gallus.
REFERENCE
AUTHORS         Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezubov,Y., Zaim,J.,
                Fiedler,P., Kutter,S., Biagodatski,A., Kostovska,D., Koter,M.,
                Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.
TITLE           Full-length cDNAs from chicken bursal lymphocytes to facilitate
                gene function analysis
JOURNAL         Genome Biol. 6 (1), R6 (2005)
PUBMED         15642098
COMMENT         Contact: Caldwell RB
                GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie
                Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.

FEATURES
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/note="CB inbred strain"

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCCCTT 16
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Db 4 CGCCCTT 10

RESULT 5
AJ591555
LOCUS
DEFINITION      10 bp DNA linear GSS 15-JAN-2004
                Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                S87C11, genomic survey sequence.
ACCESSION      AJ591555
VERSION        AJ591555.1 GI:37941179
KEYWORDS       GSS; left border; T-DNA flanking sequence.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS         Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
                Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
                Lepiniec,L., Caboche,M. and Leclercq,A.
TITLE           T-DNA integration into the Arabidopsis genome depends on sequences
                of pre-insertion sites
JOURNAL         EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED         12446565
REFERENCE
AUTHORS         Balzerque,S.
                Direct Submission
TITLE           Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
                Gaston Cremieux, 91057 Evry cedex, FRANCE
JOURNAL         PCR was performed on DNA from transformants of Arabidopsis thaliana
                plants from INRA (Versailles). The DNA fragment(s) resulting from
                the PCR were directly sequenced from the left or the right border
                to determine the genomic sequence flanking the insertion. T-DNA
                derived sequences were removed. Information to order the
                corresponding mutant line and a link to a database providing a
                graphical display of the insertion site are available at

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rosids; eurosids II; Malvales; Malvaceae; Byttnerioideae;
Theobroma.
1 (bases 1 to 10)
Jones,P.G., Allaway,D., Gilmour,D.M., Harris,C., Rankin,D.,
Retzel,E.R. and Jones,C.A.
Gene discovery and microarray analysis of cacao (Theobroma cacao
L.) varieties
Planta 216 (2), 255-264 (2002)
PUBMED 12447539
COMMENT Contact: Jones, Paul
                MasterFoods
                3d Dundee Road, Slough, Berkshire, UK, SL1 4LG
                Tel: +44 1664 416644
                Email: Paul.Jones@eu.affem.com
                Seq primer: T3.
FEATURES
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/clone_lib="Cac_BL (Bean and Leaf from Amelonardo type
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/note="Vector: pBK-CMV; Bean and leaf tissue from an
                Amelonado type Cacao tree."

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 CGCCCTT 16
    |||||
Db 4 CGCCCTT 10

RESULT 5
AJ591555
LOCUS
DEFINITION      10 bp DNA linear GSS 15-JAN-2004
                Arabidopsis thaliana T-DNA flanking sequence, left border, clone
                S87C11, genomic survey sequence.
ACCESSION      AJ591555
VERSION        AJ591555.1 GI:37941179
KEYWORDS       GSS; left border; T-DNA flanking sequence.
SOURCE         Arabidopsis thaliana (thale cress)
ORGANISM       Arabidopsis thaliana
                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
                rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE
AUTHORS         Brunaud,V., Balzerque,S., Dubreucq,B., Aubourg,S., Samson,F.,
                Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
                Lepiniec,L., Caboche,M. and Leclercq,A.
TITLE           T-DNA integration into the Arabidopsis genome depends on sequences
                of pre-insertion sites
JOURNAL         EMBO Rep. 3 (12), 1152-1157 (2002)
PUBMED         12446565
REFERENCE
AUTHORS         Balzerque,S.
                Direct Submission
TITLE           Submitted (23-OCT-2003) Balzerque S., UMRGV, INRA/CNRS, 2 rue
                Gaston Cremieux, 91057 Evry cedex, FRANCE
JOURNAL         PCR was performed on DNA from transformants of Arabidopsis thaliana
                plants from INRA (Versailles). The DNA fragment(s) resulting from
                the PCR were directly sequenced from the left or the right border
                to determine the genomic sequence flanking the insertion. T-DNA
                derived sequences were removed. Information to order the
                corresponding mutant line and a link to a database providing a
                graphical display of the insertion site are available at

```

<http://dbgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genopianté' (<http://www.genopiante.com> and <http://genopiante-info.infobiogen.fr>).

FEATURES
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 /ecotype="Wassilewskija"
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 1..10
 /note="T-DNA flanking sequence
 left border"

Query Match 26.9% Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTC 7
 |||||
Db 4 CCACCTC 10

Search completed: May 9, 2006, 16:50:29
Job time : 0.001 secs

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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

Run on: May 9, 2006, 16:58:22 ; Search time 0.001 Seconds
(without alignments)
163.436 Million cell updates/sec

Title: US-09-904-968A-4-COPY

Perfect score: 26

Sequence: 1 ccacctcgcgccttccttaagcat 26

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 283 seqs, 3143 residues

Total number of hits satisfying chosen parameters: 566

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 284 summaries

Database : ge4db4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	12.2	46.9	17	1	ACCESSION:AR456565
C 6	12.2	46.9	17	1	ACCESSION:AR463878
C 7	12.2	46.9	17	1	ACCESSION:AX217105
8	10.8	41.5	15	1	ACCESSION:CS005007
9	10.8	41.5	15	1	ACCESSION:CS005022
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11	10.8	41.5	15	1	ACCESSION:CS005071
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 C 284 7.4 28.5 10 1 BD007887 ACCESSION:BD007887

ALIGNMENTS

RESULT 1
 AX440500
 LOCUS AX440500 26 bp DNA linear PAT 28-JUN-2002
 DEFINITION Sequence 4 from Patent WO0206529.
 ACCESSION AX440500
 VERSION AX440500.1 GI:21665303
 KEYWORDS synthetic construct
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.
 REFERENCE 1
 AUTHORS Germino,G.G., Watnick,T.J. and Phakdeekitcharoen,B.
 TITLE Detection and treatment of polycystic kidney disease
 JOURNAL Patent: WO 0206529-A 4 24-JAN-2002;
 The Johns Hopkins University School of Medicine (US)
 FEATURES
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 1. .26
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="PCR primer BPR9"
 Query Match 100.0%; Score 26; DB 1; Length 26;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCACCTCATCGCCCTTCCTAAGCAT 26
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 Db 1 CCACCTCATCGCCCTTCCTAAGCAT 26
 RESULT 2
 AR492979
 LOCUS AR492979 18 bp DNA linear PAT 15-MAY-2004
 DEFINITION Sequence 11 from patent US 6720137.
 ACCESSION AR492979

VERSION AR492979.1 GI:47264283
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 18)
 AUTHORS Roder,M., Plaschke,J. and Ganai,M.
 TITLE Microsatellite markers for plants of the species *Triticum aestivum*
 and *Triticum triticeae* and the use of said markers
 JOURNAL Patent: US 6720137-A 11 13-APR-2004;
 Institut fur Pflanzengenetik und Kulturpflanzenforschung;
 Gatersleben;
 DEX;
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 1. .18
 /organism="unknown"
 /mol_type="genomic DNA"
 Query Match 49.2%; Score 12.8; DB 1; Length 18;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CCACCTCATCGCCCT 16
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 Db 2 CGACCTGATCGCCCT 17
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 RESULT 3
 LOCUS CQ615502 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 242 from Patent WO0192524.
 ACCESSION CQ615502
 VERSION CQ615502.1 GI:41665720
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Gu,Y., Ji,Y., Penn,S.G., Hanzel,D.K., Rank,D.R., Chen,W. and
 Shannon,M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 242 06-DEC-2001;
 Aeomica, Inc. (US)
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 1. .17
 /organism="Homo sapiens"
 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"
 Query Match 46.9%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 20;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 4 CCTCATCGCCCTTCCT 20
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 Db 1 CATCTCGCCCTTCCT 17
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 RESULT 4
 LOCUS CQ622815/c 17 bp DNA linear PAT 02-FEB-2004
 DEFINITION Sequence 7555 from Patent WO0192524.
 ACCESSION CQ622815
 VERSION CQ622815.1 GI:41673033
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 REFERENCE 1
 AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Hominidae; Homo.

AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Myosin-like gene expressed in human heart and muscle
 JOURNAL Patent: WO 0192524-A 7555 06-DEC-2001;
 Aeomica, Inc. (US)

FEATURES
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 1. .17
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 /mol_type="unassigned DNA"
 /db_xref="taxon:9606"

Query Match 46.9%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 20;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 TCGCCCTTCCTAAGCA 25
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 Db 17 TGGCCCCGTCAATAGCA 1

RESULT 5
 LOCUS AR456565 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 242 from patent US 6686188.
 ACCESSION AR456565
 VERSION AR456565.1 GI:42691622
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.

TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 242 03-FEB-2004;
 Amersham PLC; Buckinghamshire;
 GBX;

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 /organism="unknown"
 /mol_type="genomic DNA"

Query Match 46.9%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 20;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTTCCT 20
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 Db 1 CATCTCGCCCTCCT 17

RESULT 6
 LOCUS AR463878/c 17 bp DNA linear PAT 20-FEB-2004
 DEFINITION Sequence 7555 from patent US 6686188.
 ACCESSION AR463878
 VERSION AR463878.1 GI:42698935
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 17)
 AUTHORS Gu, Y., Ji, Y., Penn, S.G., Hanzel, D.K., Rank, D.R., Chen, W. and Shannon, M.E.
 TITLE Polynucleotide encoding a human myosin-like polypeptide expressed predominantly in heart and muscle
 JOURNAL Patent: US 6686188-A 7555 03-FEB-2004;
 Amersham PLC; Buckinghamshire;
 GBX;

FEATURES
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 Location/Qualifiers
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 /organism="unknown"

/mol_type="genomic DNA"

Query Match 46.9%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 20;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 TCGCCCTTCCTAAGCA 25
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 Db 17 TGGCCCCGTCAATAGCA 1

RESULT 7
 LOCUS AX217105/c 17 bp RNA linear PAT 07-SEP-2001
 DEFINITION Sequence 2547 from Patent WO0159103.
 ACCESSION AX217105
 VERSION AX217105.1 GI:15527166
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM other sequences; artificial sequences.

REFERENCE 1
 AUTHORS Blatt, L., McSwiggen, J. and Chowrira, B. M.
 TITLE Method and reagent for the modulation and diagnosis of cd20 and nogo gene expression
 JOURNAL Patent: WO 0159103-A 2547 16-AUG-2001;
 RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ; McSwiggen, James (US) ; Chowrira, Bharat M. (US)

FEATURES
 Location/Qualifiers
 1. .17
 source
 /organism="synthetic construct"
 /mol_type="unassigned RNA"
 /db_xref="taxon:32630"
 /note="Nucleic Acid"

Query Match 46.9%; Score 12.2; DB 1; Length 17;
 Best Local Similarity 82.4%; Pred. No. 20;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 CTCATCGCCCTTCCTA 21
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 Db 17 CTCATGGCCTCTTCATA 1

RESULT 8
 LOCUS CS005007 15 bp DNA linear PAT 07-FEB-2005
 DEFINITION Sequence 3035 from Patent EP1502950.
 ACCESSION CS005007
 VERSION CS005007.1 GI:58740362
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified

REFERENCE 1
 AUTHORS Stinchcomb, D.T., Chowrira, B., Direnzo, A., Draper, K.G., Dudycz, L.W., Grimm, S., Karpeisky, A., Kisich, K., Matulic-Adamic, J., McSwiggen, J.A., Modak, A., Pavco, P., Beigelman, L., Sullivan, S.M., Sweedler, D., Thompson, J.D., Tracz, D., Usman, N., Wincott, F.E. and Woolf, T.
 TITLE Method for purifying chemically modified RNA
 JOURNAL Patent: EP 1502950-A 3035 02-FEB-2005;
 Ribozyne Pharmaceuticals, Inc. (US)

FEATURES
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 1. .15
 /organism="unidentified"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32644"

Query Match 41.5%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	11	GCCCTTCCTAAGC 24			
Db	1	GTCCCTTCTCAGC 14			
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RESULT 9					
CS005022					
LOCUS			15 bp	DNA	linear PAT 07-FEB-2005
DEFINITION		Sequence 3050 from Patent EP1502950.			
ACCESSION		CS005022			
VERSION		CS005022.1 GI:58740377			
KEYWORDS					
SOURCE		unidentified			
ORGANISM		unclassified			
REFERENCE					
AUTHORS		Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulich-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.			
TITLE		Method for purifying chemically modified RNA			
JOURNAL		Patent: EP 1502950-A 3050 02-FEB-2005;			
FEATURES		Ribozyme Pharmaceuticals, Inc. (US)			
source		Location/Qualifiers			
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		/mol_type="unassigned DNA"			
		/db_xref="taxon:32644"			
Query Match		41.5%; Score 10.8; DB 1; Length 15;			
Best Local Similarity		85.7%; Pred. No. 34;			
Matches	12;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	1	CACCTCATCGCCC 14			
Db	2	CCACTCACGGCC 15			
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RESULT 10					
CS005061					
LOCUS			15 bp	DNA	linear PAT 07-FEB-2005
DEFINITION		Sequence 3089 from Patent EP1502950.			
ACCESSION		CS005061			
VERSION		CS005061.1 GI:58740416			
KEYWORDS					
SOURCE		unidentified			
ORGANISM		unclassified			
REFERENCE					
AUTHORS		Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulich-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.			
TITLE		Method for purifying chemically modified RNA			
JOURNAL		Patent: EP 1502950-A 3089 02-FEB-2005;			
FEATURES		Ribozyme Pharmaceuticals, Inc. (US)			
source		Location/Qualifiers			
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		/organism="unidentified"			
		/mol_type="unassigned DNA"			
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Query Match		41.5%; Score 10.8; DB 1; Length 15;			
Best Local Similarity		85.7%; Pred. No. 34;			
Matches	12;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	11	GCCCTTCCTAAGC 24			
Db	1	GTCCCTTCTCAGC 14			
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RESULT 11					
CS005071					
LOCUS			15 bp	DNA	linear PAT 07-FEB-2005
DEFINITION		Sequence 3099 from Patent EP1502950.			
ACCESSION		CS005071			
VERSION		CS005071.1 GI:58740426			
KEYWORDS					
SOURCE		unidentified			
ORGANISM		unclassified			
REFERENCE					
AUTHORS		Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulich-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.			
TITLE		Method for purifying chemically modified RNA			
JOURNAL		Patent: EP 1502950-A 3099 02-FEB-2005;			
FEATURES		Ribozyme Pharmaceuticals, Inc. (US)			
source		Location/Qualifiers			
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		/mol_type="unassigned DNA"			
		/db_xref="taxon:32644"			
Query Match		41.5%; Score 10.8; DB 1; Length 15;			
Best Local Similarity		85.7%; Pred. No. 34;			
Matches	12;	Conservative 0; Mismatches 2; Indels 0; Gaps 0;			
Qy	11	GCCCTTCCTAAGC 24			
Db	2	GTCCCTTCTCAGC 15			
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RESULT 12					
CS005079					
LOCUS			15 bp	DNA	linear PAT 07-FEB-2005
DEFINITION		Sequence 3107 from Patent EP1502950.			
ACCESSION		CS005079			
VERSION		CS005079.1 GI:58740434			
KEYWORDS					
SOURCE		unidentified			
ORGANISM		unclassified			
REFERENCE					
AUTHORS		Stinchcomb,D.T., Chowrira,B., Drenzo,A., Draper,K.G., Dudycz,L.W., Grimm,S., Karpeisky,A., Kisich,K., Matulich-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.			
TITLE		Method for purifying chemically modified RNA			
JOURNAL		Patent: EP 1502950-A 3107 02-FEB-2005;			
FEATURES		Ribozyme Pharmaceuticals, Inc. (US)</			

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VERSION      I61479.1  GI:2479427
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 15)
AUTHORS      Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE        Rel a targeted ribozymes
JOURNAL      Patent: US 5658780-A 33 19-AUG-1997;
FEATURES     Location/Qualifiers
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              /organism="unknown"
              /mol_type="unassigned DNA"

Query Match      41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGGCC 14
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Db 2 CCACCTCACCGGCC 15

RESULT 14
LOCUS      I61572
DEFINITION Sequence 126 from patent US 5658780.
ACCESSION  I61572
VERSION     I61572.1  GI:2479520
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE      Rel a targeted ribozymes
JOURNAL    Patent: US 5658780-A 126 19-AUG-1997;
FEATURES   Location/Qualifiers
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            /organism="unknown"
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Query Match      41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTCTAAGC 24
    |||||
Db 1 GTCCCTTCTCTCAGC 14

RESULT 15
LOCUS      I61599
DEFINITION Sequence 153 from patent US 5658780.
ACCESSION  I61599
VERSION     I61599.1  GI:2479547
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE      Rel a targeted ribozymes
JOURNAL    Patent: US 5658780-A 153 19-AUG-1997;
FEATURES   Location/Qualifiers
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Query Match      41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTCTAAGC 24
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Db 1 GTCCCTTCTCTCAGC 14

RESULT 16
LOCUS      I61604
DEFINITION Sequence 158 from patent US 5658780.
ACCESSION  I61604
VERSION     I61604.1  GI:2479552
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE      Rel a targeted ribozymes
JOURNAL    Patent: US 5658780-A 158 19-AUG-1997;
FEATURES   Location/Qualifiers
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Query Match      41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCCTTCTCTAAGC 24
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Db 2 GTCCCTTCTCTCAGC 15

RESULT 17
LOCUS      I61608
DEFINITION Sequence 162 from patent US 5658780.
ACCESSION  I61608
VERSION     I61608.1  GI:2479556
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unclassified.
REFERENCE  1 (bases 1 to 15)
AUTHORS    Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
TITLE      Rel a targeted ribozymes
JOURNAL    Patent: US 5658780-A 162 19-AUG-1997;
FEATURES   Location/Qualifiers
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            /mol_type="unassigned DNA"

Query Match      41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGCCCTTCTCT 20
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Db 2 CATGGTCCCTTCTCT 15

RESULT 18
LOCUS      AX635896
DEFINITION Sequence 3035 from Patent EP1260586.
ACCESSION  AX635896
VERSION     AX635896.1  GI:28471510
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unidentified
REFERENCE  1 unclassified sequences.

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AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 3035 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

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 /mol_type="unassigned RNA"
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Query Match 41.5%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCCTAAGC 24
 | ||||| |||
 Db 1 GTCCTTCCTCAGC 14

RESULT 19
 AX635911
 LOCUS 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 3050 from Patent EP1260586.
 ACCESSION AX635911
 VERSION AX635911.1 GI:28471525
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE
 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 3050 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

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 1. .15
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 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 41.5%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCC 14
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 Db 2 CCACCTCACCAGC 15

RESULT 20
 AX635950
 LOCUS 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 3089 from Patent EP1260586.
 ACCESSION AX635950
 VERSION AX635950.1 GI:28471564
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE
 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

AUTHORS Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 3089 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
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Query Match 41.5%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCCTAAGC 24
 | ||||| |||
 Db 1 GTCCTTCCTCAGC 14

RESULT 21
 AX635960
 LOCUS 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 3099 from Patent EP1260586.
 ACCESSION AX635960
 VERSION AX635960.1 GI:28471574
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE
 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

JOURNAL Patent: EP 1260586-A 3099 27-NOV-2002; RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES
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 /mol_type="unassigned RNA"
 /db_xref="taxon:32644"

Query Match 41.5%; Score 10.8; DB 1; Length 15;
 Best Local Similarity 85.7%; Pred. No. 34;
 Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCCTAAGC 24
 | ||||| |||
 Db 2 GTCCTTCCTCAGC 15

RESULT 22
 AX635968
 LOCUS 15 bp RNA linear PAT 21-FEB-2003
 DEFINITION Sequence 3107 from Patent EP1260586.
 ACCESSION AX635968
 VERSION AX635968.1 GI:28471582
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified sequences.

REFERENCE
 1
AUTHORS Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Drenzo,A., Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J., McSwiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M., Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and Woolf,T.

TITLE Method and reagent for inhibiting the expression of disease related genes

```

genes
JOURNAL Patent: EP 1260586-A 3107 27-NOV-2002;
RIBOZYME PHARMACEUTICALS, INC. (US)
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1. .15
/organism="unidentified"
/mol_type="unassigned RNA"
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Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 85.7%; Pred. No. 34;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATGCCCTTCCT 20
Db 2 CATGGTCCCTTCCT 15

RESULT 23
A89148
LOCUS 13 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1296 from Patent WO9833904.
ACCESSION A89148
VERSION A89148.1 GI:6737718
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Brysch,W. and Schlingensiepen,K.
TITLE AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL Patent: WO 9833904-A 1296 06-AUG-1998;
BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES
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1. .13
/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAAGC 24
Db 1 CTCCTTCCTAAGC 13

RESULT 24
BD066661
LOCUS 13 bp DNA linear PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION BD066661
VERSION BD066661.1 GI:22612264
KEYWORDS JP 2001511000-A/1296.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 13)
AUTHORS Schlingensiepen,K.H. and Brysch,W.
TITLE An antisense oligonucleotide preparation method
JOURNAL Patent: JP 2001511000-A 1296 07-AUG-2001;
BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT OS Unknown
PN JP 2001511000-A/1296
PD 07-AUG-2001
PF 30-JAN-1998 JP 1998532533
PR 31-JAN-1997 EP 97101331.8
PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
PC C12N15/11,C07H21/04,A61K31/70
CC An antisense oligonucleotide preparation method FH Key
Location/Qualifiers
1. .13
/organism="unidentified"
/db_xref="taxon:32644"

FT source
/organism="unidentified"
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/db_xref="taxon:32644"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAAGC 24
Db 1 CTCCTTCCTAAGC 13

RESULT 25
AR637821/c
LOCUS 13 bp DNA linear PAT 20-APR-2005
DEFINITION Sequence 35 from patent US 6855866.
ACCESSION AR637821
VERSION AR637821.1 GI:62771643
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 13)
AUTHORS Weterings,K., Apuya,N.R. and Goldberg,R.B.
TITLE Polynucleotides useful for modulating transcription
JOURNAL Patent: US 6855866-A 35 15-FEB-2005;
The Regents of the University of California; Oakland, CA
FEATURES
source
1. .13
/organism="unidentified"
/mol_type="genomic DNA"

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 46;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCTTAAGCAT 26
Db 13 CTTTCATAAGCTT 1

RESULT 26
AX627110/c
LOCUS 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4151 from Patent WO02053774.
ACCESSION AX627110
VERSION AX627110.1 GI:28455148
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4151 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 ATCGCCCTTC 18

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Db      11  |||||
          |||
          11  ATGCCCTTC 1

RESULT 27
AX627937
LOCUS      AX627937      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4978 from Patent WO02053774.
ACCESSION  AX627937
VERSION     AX627937.1  GI:28455975
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4978 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2  CACCTCATCCG 12
          |||||
          1  CACCTCATCC 11

RESULT 28
AX629196/c
LOCUS      AX629196      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6237 from Patent WO02053774.
ACCESSION  AX629196
VERSION     AX629196.1  GI:28457234
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6237 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
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              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      36.2%; Score 9.4; DB 1; Length 11;
Best Local Similarity 90.9%; Pred. No. 46;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15  CTTCTCAAGCA 25
          |||||
          11  CTTCTCAGCA 1

RESULT 29
A89149
LOCUS      A89149      13 bp      DNA      linear      PAT 22-JAN-2000
DEFINITION Sequence 1297 from Patent WO9833904.
ACCESSION  A89149

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VERSION     A89149.1  GI:6737719
KEYWORDS    .
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 13)
AUTHORS     Brysch,W. and Schlingensiepen,K.
TITLE       AN ANTISENSE OLIGONUCLEOTIDE PREPARATION METHOD
JOURNAL     Patent: WO 9833904-A 1297 06-AUG-1998;
            BIOGNOSTIK GES (DE); BRYSCH WOLFGANG (DE)
FEATURES   Location/Qualifiers
            source
              1..13
              /organism="unidentified"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32644"

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14  CCTTCCTAAGC 24
          |||||
          1  CCTTCCTAAGC 11

RESULT 30
BD066662
LOCUS      BD066662      13 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION An antisense oligonucleotide preparation method.
ACCESSION  BD066662
VERSION     BD066662.1  GI:22612265
KEYWORDS    JP 2001511000-A/1297.
SOURCE      unidentified
ORGANISM    unidentified
REFERENCE   1 (bases 1 to 13)
AUTHORS     Schlingensiepen,K.H. and Brysch,W.
TITLE       An antisense oligonucleotide preparation method
JOURNAL     Patent: JP 2001511000-A 1297 07-AUG-2001;
            BIOGNOSTIK GESELLSCHAFT FUR BIOMOLEKULARE DIAGNOSTIK MBH
COMMENT     OS Unknown
            PN JP 2001511000-A/1297
            PD 07-AUG-2001
            PE 30-JAN-1998 JP 1998532533
            PR 31-JAN-1997 EP 97101531.8
            PI KARL HERMANN SCHLINGENSIEPEN,WOLFGANG BRYSCH
            PC C12N15/11,C07H21/04,A61K31/70
            CC An antisense oligonucleotide preparation method FH Key
            Location/Qualifiers
            FT source
              1..13
              /organism='Unknown'.
              Location/Qualifiers
                1..13
                /organism="unidentified"
                /mol_type="genomic DNA"
                /db_xref="taxon:32644"

Query Match      36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 55;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      14  CCTTCCTAAGC 24
          |||||
          1  CCTTCCTAAGC 11

RESULT 31
BD091501
LOCUS      BD091501      13 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Transcriptional activator.
ACCESSION  BD091501
KEYWORDS    BD091501.1  GI:22637112
            WO 0132860-A/2.

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BD105402/C
LOCUS          BD105402              10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same.
ACCESSION      BD105402
VERSION        BD105402.1 GI:22650976
KEYWORDS       JP 2001348398-A/2.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Saito, I., Fujimoto, K., Matsuda, S. and Yoshino, H.
TITLE          5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same
JOURNAL        Patent: JP 2001348398-A 2 18-DEC-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        PN JP 2001348398-A/2
PD 18-DEC-2001
PF 05-JAN-2001 JP 2001000750
PI ISAO SAITO, KENZO FUJIMOTO, SHIGEO MATSUDA, HIDEAKI YOSHINO PC
C07H21/04, C07H1/00, C07H19/10, C12P19/30, C12Q1/68 CC Description of
Artificial Sequence: template DNA; named ODN A3 FH Key
Location/Qualifiers
FT source      1..10
FT             Location/Qualifiers
FEATURES       source
               1..10
               /organism="Artificial Sequence".
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match    34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGCA 25
Db 9 TCCTAAGCA 1

RESULT 37
LOCUS          BD240558              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Preparation and use of superior vaccines.
ACCESSION      BD240558
VERSION        BD240558.1 GI:33050328
KEYWORDS       JP 2002534056-A/1976.
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Roberts, B.L. and Shankara, S.
TITLE          Preparation and use of superior vaccines
JOURNAL        Patent: JP 2002534056-A 1976 15-OCT-2002;
GENZYME CORP
COMMENT        OS Homo sapiens (human)
PN JP 2002534056-A/1976
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR

BD105402
LOCUS          BD105402              10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION     5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same.
ACCESSION      BD105402
VERSION        BD105402.1 GI:22650976
KEYWORDS       JP 2001348398-A/2.
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Saito, I., Fujimoto, K., Matsuda, S. and Yoshino, H.
TITLE          5-Pyrimidine-containing nucleic acid, and reversible ligation
method using the same
JOURNAL        Patent: JP 2001348398-A 2 18-DEC-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        PN JP 2001348398-A/2
PD 18-DEC-2001
PF 05-JAN-2001 JP 2001000750
PI ISAO SAITO, KENZO FUJIMOTO, SHIGEO MATSUDA, HIDEAKI YOSHINO PC
C07H21/04, C07H1/00, C07H19/10, C12P19/30, C12Q1/68 CC Description of
Artificial Sequence: template DNA; named ODN A3 FH Key
Location/Qualifiers
FT source      1..10
FT             Location/Qualifiers
FEATURES       source
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               /organism="Artificial Sequence".
               /organism="synthetic construct"
               /mol_type="genomic DNA"
               /db_xref="taxon:32630"

Query Match    34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGCA 25
Db 9 TCCTAAGCA 1

RESULT 37
LOCUS          BD240558              10 bp      DNA      linear      PAT 17-JUL-2003
DEFINITION     Preparation and use of superior vaccines.
ACCESSION      BD240558
VERSION        BD240558.1 GI:33050328
KEYWORDS       JP 2002534056-A/1976.
SOURCE         Homo sapiens (human)
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1 (bases 1 to 10)
AUTHORS        Roberts, B.L. and Shankara, S.
TITLE          Preparation and use of superior vaccines
JOURNAL        Patent: JP 2002534056-A 1976 15-OCT-2002;
GENZYME CORP
COMMENT        OS Homo sapiens (human)
PN JP 2002534056-A/1976
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039, 19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041, 19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997, 19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035, 19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992, 19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878, 19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000, 19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999, 19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042, 19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044, 19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080, 19-JUN-1998 US 60/089833 PR

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19-JUN-1998 US 60/089994, 19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078, 19-JUN-1998 US 60/090047 PR
19-JUN-1998 US 60/090076, 19-JUN-1998 US 60/090045 PR
08-DSC-1998 US 60/111715
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/09, A61K39/00, A61P35/00, A61P37/04, C12N1/15, PC
C12N1/19,
PC C12N1/21, C12N5/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
G01N37/00.
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source      1..10
FT             Location/Qualifiers
FEATURES       source
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               /organism="Homo sapiens"
               /mol_type="genomic DNA"
               /db_xref="taxon:9606"

Query Match    34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTCCTAAG 23
Db 2 CTCCTAAG 10

RESULT 38
LOCUS          CQ837376              11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION     Sequence 2434 from Patent WO2004059001.
ACCESSION      CQ837376
VERSION        CQ837376.1 GI:50836910
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS        Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
Conradt, M. and Hofmann, K.
TITLE          Method for determining markers of human facial skin
JOURNAL        Patent: WO 2004059001-A 2434 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES       source
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               /organism="Homo sapiens"
               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match    34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 3 CCCCTTCCT 11

RESULT 39
LOCUS          CQ837875              11 bp      DNA      linear      PAT 29-JUL-2004
DEFINITION     Sequence 2933 from Patent WO2004059001.
ACCESSION      CQ837875
VERSION        CQ837875.1 GI:50837409
KEYWORDS       .
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

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Db      11 CCACCTCAT 3

RESULT 44
AX628454
LOCUS      AX628454          11 bp  DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5495 from Patent WO02053774.
ACCESSION  AX628454
VERSION     AX628454.1 GI:28456492
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 5495 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
Db      3 CCCCTTCCT 11

RESULT 45
AX630822
LOCUS      AX630822          11 bp  DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7863 from Patent WO02053774.
ACCESSION  AX630822
VERSION     AX630822.1 GI:28458862
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 7863 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
Db      3 CCCCTTCCT 11

RESULT 46
AX631202
LOCUS      AX631202          11 bp  DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 8244 from Patent WO02053774.
ACCESSION  AX631202

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VERSION  AX631202.1 GI:28459246
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 8244 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
Db      3 CCCCTTCCT 11

RESULT 47
AX632353/c
LOCUS      AX632353          11 bp  DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 9395 from Patent WO02053774.
ACCESSION  AX632353
VERSION     AX632353.1 GI:28467968
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

REFERENCE
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 9395 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      34.6%; Score 9; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 CCCCTTCCT 20
Db      3 CCCCTTCCT 11

RESULT 48
AX71544
LOCUS      AX71544          12 bp  DNA      linear      PAT 07-MAY-1999
DEFINITION Sequence 103 from Patent W09013521.
ACCESSION  AX71544
VERSION     AX71544.1 GI:4775156
KEYWORDS   .
SOURCE     unidentified
ORGANISM   unclassified sequences.
            1 (bases 1 to 12)
REFERENCE  Fesce,R. and Consalez,G.
AUTHORS    METHOD FOR THE DIFFERENTIAL SCREENING OF GENE EXPRESSION BY RANDOM
            PRIMED REVERSE TRANSCRIPTION-POLYMERASE CHAIN REACTION
            TITLE

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JOURNAL	Patent: WO 9813521-A 103 02-APR-1998;
FEATURES	FESCE RICCARDO (IT)
source	Location/Qualifiers
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	/mol_type="unassigned DNA"
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Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	2 CACCTCATGCC 13
Db	1 CGCCTCATTGCC 12
RESULT 49	
LOCUS	AR024081
DEFINITION	Sequence 31 from patent US 5795778.
ACCESSION	AR024081
VERSION	AR024081.1 GI:3977375
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Draper,K.G.
TITLE	Method and reagent for inhibiting herpes simplex virus replication
JOURNAL	Patent: US 5795778-A 31 18-AUG-1998;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	4 CCTCATCGCCCC 15
Db	1 CCTCCAGGCCCC 12
RESULT 50	
LOCUS	AR030073
DEFINITION	Sequence 262 from patent US 5861244.
ACCESSION	AR030073
VERSION	AR030073.1 GI:5943287
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Wang,C.-G. and Hepburn,A.G.
TITLE	Genetic sequence assay using DNA triple strand formation
JOURNAL	Patent: US 5861244-A 262 19-JAN-1999;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	4 CCTCATCGCCCC 15
Db	1 CCTCTTCCCCC 12
JOURNAL	Patent: WO 9813521-A 103 02-APR-1998;
FEATURES	FESCE RICCARDO (IT)
source	Location/Qualifiers
	1..12
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	2 CACCTCATGCC 13
Db	1 CGCCTCATTGCC 12
RESULT 49	
LOCUS	AR024081
DEFINITION	Sequence 31 from patent US 5795778.
ACCESSION	AR024081
VERSION	AR024081.1 GI:3977375
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Draper,K.G.
TITLE	Method and reagent for inhibiting herpes simplex virus replication
JOURNAL	Patent: US 5795778-A 31 18-AUG-1998;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	4 CCTCATCGCCCC 15
Db	1 CCTCCAGGCCCC 12
RESULT 50	
LOCUS	AR030073
DEFINITION	Sequence 262 from patent US 5861244.
ACCESSION	AR030073
VERSION	AR030073.1 GI:5943287
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Wang,C.-G. and Hepburn,A.G.
TITLE	Genetic sequence assay using DNA triple strand formation
JOURNAL	Patent: US 5861244-A 262 19-JAN-1999;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	4 CCTCATCGCCCC 15
Db	1 CCTCTTCCCCC 12
JOURNAL	Patent: WO 9813521-A 103 02-APR-1998;
FEATURES	FESCE RICCARDO (IT)
source	Location/Qualifiers
	1..12
	/organism="unidentified"
	/mol_type="unassigned DNA"
	/db_xref="taxon:32644"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	2 CACCTCATGCC 13
Db	1 CGCCTCATTGCC 12
RESULT 49	
LOCUS	AR024081
DEFINITION	Sequence 31 from patent US 5795778.
ACCESSION	AR024081
VERSION	AR024081.1 GI:3977375
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Draper,K.G.
TITLE	Method and reagent for inhibiting herpes simplex virus replication
JOURNAL	Patent: US 5795778-A 31 18-AUG-1998;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	4 CCTCATCGCCCC 15
Db	1 CCTCCAGGCCCC 12
RESULT 50	
LOCUS	AR030073
DEFINITION	Sequence 262 from patent US 5861244.
ACCESSION	AR030073
VERSION	AR030073.1 GI:5943287
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 12)
AUTHORS	Wang,C.-G. and Hepburn,A.G.
TITLE	Genetic sequence assay using DNA triple strand formation
JOURNAL	Patent: US 5861244-A 262 19-JAN-1999;
FEATURES	Location/Qualifiers
source	1..12
	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity	83.3%; Pred. No. 67;
Matches	10; Conservative 0; Mismatches

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LOCUS      AX010703                12 bp      DNA      linear      PAT 06-SEP-2000
DEFINITION Sequence 45 from Patent WO9958655.
ACCESSION  AX010703
VERSION     AX010703.1  GI:9997496
KEYWORDS    synthetic construct
SOURCE      other sequences; artificial sequences.
ORGANISM    1
REFERENCE   1
AUTHORS     Kristensen, P., Jestin, J.L., Winter, G.P. and Riechmann, L.
TITLE       Selection system
JOURNAL     Patent: WO 9958655-A 45 18-NOV-1999;
            KRISTENSEN PETER (DK); JESTIN JEAN LUC (FR); MEDICAL RES COUNCIL
            (GB); WINTER GREGORY PAUL (GB); RIECHMANN LUTZ (GB)
FEATURES    Location/Qualifiers
             1..12
             /organism="synthetic construct"
             /mol_type="unassigned DNA"
             /db_xref="taxon:32630"
             /note="PRIMER"
Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGC 12
Db 12 CCACATCTTGGC 1

RESULT 54
AX711075
LOCUS      AX711075                12 bp      RNA      linear      PAT 11-APR-2003
DEFINITION Sequence 375 from Patent EP1288296.
ACCESSION  AX711075
VERSION     AX711075.1  GI:29787456
KEYWORDS    Herpes simplex virus unknown type
SOURCE      Herpes simplex virus unknown type
ORGANISM    Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
            Alphaherpesvirinae; Simplexvirus.
REFERENCE   1
AUTHORS     Draper, K.G., Mcswiggen, J.A., Holecek, J.J., Dudycz, L.W.,
            Macejak, D.G. and Mamone, A.J.
TITLE       Method and reagent for inhibiting HBV viral replication
JOURNAL     Patent: EP 1288296-A 375 05-MAR-2003;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES    Location/Qualifiers
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             /organism="Herpes simplex virus unknown type"
             /mol_type="unassigned RNA"
             /db_xref="taxon:126283"
Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 1 CTCACGCCCC 12

RESULT 55
BD001185
LOCUS      BD001185                12 bp      RNA      linear      PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION  BD001185
VERSION     BD001185.1  GI:18625744
KEYWORDS    synthetic construct
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 12)

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AUTHORS     Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
            Holecek, J.J. and Mamone, A.J.
TITLE       Method and reagent for inhibiting viral replication
JOURNAL     Patent: JP 2000342285-A 345 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS Artificial Sequence
            PN JP 2000342285-A/345
            PD 12-DEC-2000
            PF 01-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
            PR 11-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
            14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
            14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
            14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
            14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/883823 PR
            14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884073 PR
            14-MAY-1992 US 07/884074, 14-MAY-1992 US 07/884333 PR
            14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
            14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
            31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
            26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
            15-OCT-1992 US 07/963222, 07-DEC-1992 US 07/987129 PR
            07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
            KENNETH G DRAPER, DEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
            MAYSEJAK,
            PI JAMES J HOLESEK, ANTHONY J MAMONE
            PC C12N15/09, C12N5/10, C12N7/00, C12N9/22// (C12N5/10, C12R1:91), PC
            C12N15/00,
            PC C12N5/00, (C12N5/00, C12R1:91)
            CC
            FT Key source 1..12 Location/Qualifiers
            PT /organism="Artificial Sequence".
FEATURES    source
             1..12
             /organism="synthetic construct"
             /mol_type="genomic RNA"
             /db_xref="taxon:32630"
Query Match      33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
Db 1 CTCACGCCCC 12

RESULT 56
BD001614
LOCUS      BD001614                12 bp      RNA      linear      PAT 31-JAN-2002
DEFINITION Method and reagent for inhibiting viral replication.
ACCESSION  BD001614
VERSION     BD001614.1  GI:18626173
KEYWORDS    JP 2000342286-A/345.
SOURCE      synthetic construct
ORGANISM    synthetic construct
            other sequences; artificial sequences.
REFERENCE   1 (bases 1 to 12)
AUTHORS     Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
            Holecek, J.J. and Mamone, A.J.
TITLE       Method and reagent for inhibiting viral replication
JOURNAL     Patent: JP 2000342286-A 345 12-DEC-2000;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS Artificial Sequence
            PN JP 2000342286-A/345
            PD 12-DEC-2000
            PF 01-MAY-2000 JP 2000132651
            PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
            14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
            14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
            14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
            14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR

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14-MAY-1992 US 07/882922,14-MAY-1992 US 07/883823 PR
14-MAY-1992 US 07/883849,14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/884074,14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422,14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436,14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738,26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086,18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322,07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130,07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER,LEC W DADYKTZ,JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,
PI JAMES J HOLSEK,ANTHONY J MAMONE
PC C12N15/09,C12N5/10,C12N7/00//A61K38/43,A61K39/125,A61K39/13,
PC A61K39/135,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61K39/145,A61K39/21,A61K39/23,A61K39/245,A61K39/29,A61K48/00,
PC A61P1/16,
PC A61P31/14,A61P31/16,A61P31/18,A61P31/22,A61P35/02,C12Q1/68, PC
(C12N15/09,C12R1:93),C12N15/00,C12N5/00,A61K37/48,(C12N15/00, PC
C12R1:93)
CC
FH Key Location/Qualifiers
FT source 1..12
FT Location/Qualifiers
FEATURES
source
1..12
/organism="synthetic construct"
/mol_type="genomic RNA"
/db_xref="taxon:32630"
Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No.67;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 4 CCTCATCGCCCC 15
|||||
Db 1 CCTCCACGCCCC 12
RESULT 57
AR030034/c
LOCUS
DEFINITION
Sequence 223 from patent US 5861244.
ACCESSION
AR030034
VERSION
AR030034.1 GI:5943248
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Wang,C.-G. and Hepburn,A.G.
TITLE
Genetic sequence assay using DNA triple strand formation
JOURNAL
Patent: US 5861244-A 223 19-JAN-1999;
FEATURES
Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No.66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 9 TCGCCCCCTTC 18
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Db 10 TCCCCCTTC 1
RESULT 58
AR043160
LOCUS
DEFINITION
Sequence 44 from patent US 5814453.
ACCESSION
AR043160
VERSION
AR043160.1 GI:5964168
KEYWORDS

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SOURCE
ORGANISM
Unknown.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Beck,J.Joseph.
TITLE
Detection of fungal pathogens using the polymerase chain reaction
JOURNAL
Patent: US 5814453-A 44 29-SEP-1998;
FEATURES
Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No.66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 TCATCGCCCC 15
|||||
Db 1 TTATCGCCCC 10
RESULT 59
AR074660
LOCUS
DEFINITION
Sequence 44 from patent US 5955274.
ACCESSION
AR074660
VERSION
AR074660.1 GI:10001413
KEYWORDS
Unknown.
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Ligon,J.M. and Beck,J.J.
TITLE
Detection of fungal pathogens using the polymerase chain reaction
JOURNAL
Patent: US 5955274-A 44 21-SEP-1999;
FEATURES
Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No.66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 6 TCATCGCCCC 15
|||||
Db 1 TTATCGCCCC 10
RESULT 60
BD238681/c
LOCUS
DEFINITION
Preparation and use of superior vaccines.
ACCESSION
BD238681
VERSION
BD238681.1 GI:33048451
KEYWORDS
JP 2002534056-A/99.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 (bases 1 to 10)
AUTHORS
Roberts,B.I. and Shankara,S.
TITLE
Preparation and use of superior vaccines
JOURNAL
Patent: JP 2002534056-A 99 15-OCT-2002;
COMMENT
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/99
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR

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QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 66
LOCUS 122209
DEFINITION Sequence 23 from patent US 5527671.
ACCESSION 122209
VERSION 122209.1 GI:1602563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Li, K., Rouse, D.I. and German, T.L.
TITLE Assay for verticillium dahliae
JOURNAL Patent: US 5527671-A 23 18-JUN-1996;
FEATURES
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 67
LOCUS AX152425/c
DEFINITION Sequence 340 from Patent WO0138577.
ACCESSION AX152425
VERSION AX152425.1 GI:14534076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 340 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCGC 12
Db 10 ACCTCATCGC 1

RESULT 68
LOCUS AX152861/c
DEFINITION Sequence 776 from Patent WO0138577.
ACCESSION AX152861
VERSION AX152861.1 GI:14534512
KEYWORDS

QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 66
LOCUS 122209
DEFINITION Sequence 23 from patent US 5527671.
ACCESSION 122209
VERSION 122209.1 GI:1602563
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Li, K., Rouse, D.I. and German, T.L.
TITLE Assay for verticillium dahliae
JOURNAL Patent: US 5527671-A 23 18-JUN-1996;
FEATURES
source
1. .10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 67
LOCUS AX152425/c
DEFINITION Sequence 340 from Patent WO0138577.
ACCESSION AX152425
VERSION AX152425.1 GI:14534076
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 340 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCGC 12
Db 10 ACCTCATCGC 1

RESULT 68
LOCUS AX152861/c
DEFINITION Sequence 776 from Patent WO0138577.
ACCESSION AX152861
VERSION AX152861.1 GI:14534512
KEYWORDS

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 776 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTA 21
Db 10 CCCCTTCCTA 1

RESULT 69
LOCUS AX152959
DEFINITION Sequence 874 from Patent WO0138577.
ACCESSION AX152959
VERSION AX152959.1 GI:14534610
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 874 31-MAY-2001;
The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCTTCCTC 20
Db 1 GCCCTTCCTC 10

RESULT 70
LOCUS AX152960
DEFINITION Sequence 875 from Patent WO0138577.
ACCESSION AX152960
VERSION AX152960.1 GI:14534611
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 875 31-MAY-2001;

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The Johns Hopkins University (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCTCCT 20
    |||||
Db 1 GCCCCTGCTCCT 10

RESULT 71
AX153190/c
LOCUS AX153190 10 bp DNA linear PAT 22-JUN-2001
DEFINITION Sequence 1105 from Patent WO0138577.
ACCESSION AX153190
VERSION AX153190.1 GI:14534841
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
TITLE Human transcriptomes
JOURNAL Patent: WO 0138577-A 1105 31-MAY-2001;
The Johns Hopkins University (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCC 13
    |||||
Db 10 CCTCATCACC 1

RESULT 72
AX302593/c
LOCUS AX302593 10 bp DNA linear PAT 30-NOV-2001
DEFINITION Sequence 111 from Patent WO0175177.
ACCESSION AX302593
VERSION AX302593.1 GI:17383120
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1
AUTHORS Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE Tumor markers in ovarian cancer
JOURNAL Patent: WO 0175177-A 111 11-OCT-2001;
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;

The Johns Hopkins University (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 73;

The Johns Hopkins University (US)
Location/Qualifiers
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCTCCT 20
    |||||
Db 10 GCCCCTCCTCCT 1

RESULT 73
BD007795/c
LOCUS BD007795 10 bp DNA linear PAT 31-JAN-2002
DEFINITION LPS activated human monocyte expressing genes.
ACCESSION BD007795
VERSION BD007795.1 GI:18636168
KEYWORDS JP 2001069993-A/71.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
TITLE LPS activated human monocyte expressing genes
JOURNAL Patent: JP 2001069993-A 71 21-MAR-2001;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2001069993-A/71
PD 21-MAR-2001
PF 28-APR-2000 JP 2000131079
PR
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
A61P29/00,
PC A61P31/00,C12P21/08,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1. .10
FT /organism="Homo sapiens"
FT /mol_type="genomic DNA"
FT /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 66;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 CGCCCTTCTCC 19
    |||||
Db 10 CTCCTCTTCC 1

RESULT 74
AR029871
LOCUS AR029871 11 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5861244.
ACCESSION AR029871
VERSION AR029871.1 GI:5943085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 11)
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 60 19-JAN-1999;
Location/Qualifiers
1. .11
/organism="unknown"
/mol_type="unassigned DNA"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
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Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY
LOCUS      CQ832679
DEFINITION      Sequence 50 from Patent WO2004059002.
ACCESSION      CQ832679
VERSION      CQ832679.1  GI:50832286
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE      Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 50 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%;  Score 8.4;  DB 1;  Length 11;
Best Local Similarity 90.0%;  Pred. No. 73;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      11  GCCCCTTCCT 20
Db      2  GCCCCTTCCT 11

RESULT 76
CQ832959/c
LOCUS      CQ832959
DEFINITION      Sequence 330 from Patent WO2004059002.
ACCESSION      CQ832959
VERSION      CQ832959.1  GI:50832566
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE      Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 330 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%;  Score 8.4;  DB 1;  Length 11;
Best Local Similarity 90.0%;  Pred. No. 73;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      11  GCCCCTTCCT 20
Db      2  GCCCCTTCCT 11

RESULT 75
CQ832679
LOCUS      CQ832679
DEFINITION      Sequence 50 from Patent WO2004059002.
ACCESSION      CQ832679
VERSION      CQ832679.1  GI:50832286
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE      Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 50 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%;  Score 8.4;  DB 1;  Length 11;
Best Local Similarity 90.0%;  Pred. No. 73;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      10  CGCCCTTCCT 19
Db      10  CTCCCTTCCT 1

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RESULT 77
CQ833029/c
LOCUS      CQ833029
DEFINITION      Sequence 400 from Patent WO2004059002.
ACCESSION      CQ833029
VERSION      CQ833029.1  GI:50832636
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE      Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 400 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%;  Score 8.4;  DB 1;  Length 11;
Best Local Similarity 90.0%;  Pred. No. 73;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      17  TCCTAAGCAT 26
Db      11  TACTAAGCAT 2

RESULT 78
CQ835576
LOCUS      CQ835576
DEFINITION      Sequence 634 from Patent WO2004059001.
ACCESSION      CQ835576
VERSION      CQ835576.1  GI:50835110
KEYWORDS      .
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE      1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
CONRADT,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL      Patent: WO 2004059001-A 634 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES      source
Location/Qualifiers
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%;  Score 8.4;  DB 1;  Length 11;
Best Local Similarity 90.0%;  Pred. No. 73;
Matches      9;  Conservative      0;  Mismatches      1;  Indels      0;  Gaps      0;

QY      11  GCCCCTTCCT 20
Db      1  GCCCCTTCCT 10

RESULT 79
CQ836387
LOCUS      CQ836387
DEFINITION      Sequence 1445 from Patent WO2004059001.
ACCESSION      CQ836387
VERSION      CQ836387.1  GI:50835921
KEYWORDS      .

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 1445 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCCCCTTCCT 20
Db      2 GGCCTTCCT 11

RESULT 80
LOCUS    CQ836706/c
DEFINITION
Sequence 1764 from Patent WO2004059001.
ACCESSION CQ836706
VERSION   CQ836706.1 GI:50836240
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 1764 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      15 CTTCTTAAGC 24
Db      11 CATCTTAAGC 2

RESULT 81
LOCUS    CQ836926
DEFINITION
Sequence 1984 from Patent WO2004059001.
ACCESSION CQ836926
VERSION   CQ836926.1 GI:50836460
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,

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            Conradt,M. and Hofmann,K.
            Method for determining markers of human facial skin
            Patent: WO 2004059001-A 1984 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      5 CTCATCGGCC 14
Db      1 CTCACGGGCC 10

RESULT 82
LOCUS    CQ836928
DEFINITION
Sequence 1986 from Patent WO2004059001.
ACCESSION CQ836928
VERSION   CQ836928.1 GI:50836462
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 1986 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      11 GCCCCTTCCT 20
Db      2 GGCCTTCCT 11

RESULT 83
LOCUS    CQ836982/c
DEFINITION
Sequence 2040 from Patent WO2004059001.
ACCESSION CQ836982
VERSION   CQ836982.1 GI:50836516
KEYWORDS
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE       Method for determining markers of human facial skin
JOURNAL     Patent: WO 2004059001-A 2040 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
            source
              1..11
              /organism="Homo sapiens"

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/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATGCC 13
Db 10 CCTCATCTCC 1

RESULT 84
LOCUS      CQ837387/c
DEFINITION Sequence 2445 from Patent WO2004059001.
ACCESSION  CQ837387
VERSION     CQ837387.1 GI:50836921
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 2445 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCTTCTCT 20
Db 10 GCTCTTCTCT 1

RESULT 85
LOCUS      CQ837506/c
DEFINITION Sequence 2564 from Patent WO2004059001.
ACCESSION  CQ837506
VERSION     CQ837506.1 GI:50837040
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 2564 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCTTCTCT 20
Db 10 GCTCTTCTCT 1

RESULT 86
LOCUS      CQ837993/c
DEFINITION Sequence 3051 from Patent WO2004059001.
ACCESSION  CQ837993
VERSION     CQ837993.1 GI:50837527
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
            Conradt,M. and Hofmann,K.
TITLE      Method for determining markers of human facial skin
JOURNAL    Patent: WO 2004059001-A 3051 15-JUL-2004;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
Db 11 TCATCTCCCC 2

RESULT 87
LOCUS      CS058148/c
DEFINITION Sequence 45 from Patent WO2005028671.
ACCESSION  CS058148
VERSION     CS058148.1 GI:62551100
KEYWORDS   Homo sapiens (human)
SOURCE     Homo sapiens
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE  1
AUTHORS    Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
            Kessler-Becker,D.
TITLE      Method for determining hair cycle markers
JOURNAL    Patent: WO 2005028671-A 45 31-MAR-2005;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES   Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCTTCTCT 20
Db 10 GCCCTTCTCT 1

RESULT 88
AX393137/c

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LOCUS AX393137 11 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 67 from Patent WO0210217.
ACCESSION AX393137
VERSION AX393137.1 GI:19701187
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1

AUTHORS St Croix,B., Kinzler,K.W. and Vogelstein,B.

TITLE Endothelial cell expression patterns

JOURNAL Patent: WO 0210217-A 67 07-FEB-2002;

The Johns Hopkins University (US)

FEATURES Location/Qualifiers

source

1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 73;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCTTAAGC 24

| | | | |

11 CATCTTAAGC 2

RESULT 89

AX470453/c

LOCUS AX470453 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 30 from Patent WO02053773.

ACCESSION AX470453

VERSION AX470453.1 GI:22205578

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.

TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 30 11-JUL-2002;

HENKEL KGAA (DE)

FEATURES Location/Qualifiers

source

1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 73;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTA 21

| | | | |

10 CCCCATCTTA 1

RESULT 90

AX470489/c

LOCUS AX470489 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 66 from Patent WO02053773.

ACCESSION AX470489

VERSION AX470489.1 GI:22205614

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.

TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 66 11-JUL-2002;

HENKEL KGAA (DE)

FEATURES Location/Qualifiers

source

1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 73;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20

| | | | |

10 GCCCCTTCCT 1

RESULT 91

AX470678/c

LOCUS AX470678 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 255 from Patent WO02053773.

ACCESSION AX470678

VERSION AX470678.1 GI:22205803

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.

TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 255 11-JUL-2002;

HENKEL KGAA (DE)

FEATURES Location/Qualifiers

source

1..11

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;

Best Local Similarity 90.0%; Pred. No. 73;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCC 13

| | | | |

10 CCTCATCTCC 1

RESULT 92

AX471686/c

LOCUS AX471686 11 bp DNA linear PAT 09-AUG-2002

DEFINITION Sequence 1263 from Patent WO02053773.

ACCESSION AX471686

VERSION AX471686.1 GI:22206811

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

REFERENCE 1

AUTHORS Hofmann,K., Conradt,M. and Petersohn,D.

TITLE Method for determining skin stress or skin ageing in vitro

JOURNAL Patent: WO 02053773-A 1263 11-JUL-2002;

HENKEL KGAA (DE)

FEATURES Location/Qualifiers

source

1..11

/organism="Homo sapiens"

Db 10 GCCCTCCCT 1

RESULT 95
AX625417/c
LOCUS AX625417 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2458 from Patent WO02053774.
ACCESSION AX625417
VERSION AX625417.1 GI:28453358
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2458 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CCTCATCGCC 13
|||||
Db 10 CCTCATCTCC 1

RESULT 96
AX626288
LOCUS AX626288 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3329 from Patent WO02053774.
ACCESSION AX626288
VERSION AX626288.1 GI:28454326
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3329 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTCATCGCCC 14
|||||
Db 1 CTCACGCCC 10

RESULT 97
AX626376
LOCUS AX626376 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 3417 from Patent WO02053774.
ACCESSION AX626376
VERSION AX626376.1 GI:28454414
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 3417 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source 1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 CTCATCGCCC 14
|||||
Db 1 CTCACGCCC 10

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KEYWORDS      Homo sapiens (human)
SOURCE        Homo sapiens
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 3417 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCCCTTCCT 20
Db 2 GCCCTTCCT 11

RESULT 98
AX627454/c
LOCUS      AX627454      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4495 from Patent WO02053774.
ACCESSION  AX627454
VERSION     AX627454.1 GI:28455492
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 4495 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 CCCCTTCCTA 21
Db 10 CCCCTTCCTA 1

RESULT 99
AX627875/c
LOCUS      AX627875      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4916 from Patent WO02053774.
ACCESSION  AX627875
VERSION     AX627875.1 GI:28455913
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
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JOURNAL      Patent: WO 02053774-A 4916 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
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              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCATC 10
Db 10 CCACCTCATC 1

RESULT 100
AX628365
LOCUS      AX628365      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5406 from Patent WO02053774.
ACCESSION  AX628365
VERSION     AX628365.1 GI:28456403
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5406 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCCCTTCCT 20
Db 1 GCCCTTCCT 10

RESULT 101
AX628882
LOCUS      AX628882      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5923 from Patent WO02053774.
ACCESSION  AX628882
VERSION     AX628882.1 GI:28456920
KEYWORDS    .
SOURCE      Homo sapiens (human)
ORGANISM    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.
REFERENCE     1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 5923 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
              1..11
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 GCCCTTCCT 20
Db 1 GCCCTTCCT 10
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Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20
||| |||||
Db 2 GCGCCTTCCT 11

RESULT 102
AX629566/c
LOCUS AX629566 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6607 from Patent WO02053774.
ACCESSION AX629566
VERSION AX629566.1 GI:28457604
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6607 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCCGCC 15
||| |||||
Db 11 TCATCTCCCC 2

RESULT 103
AX629571/c
LOCUS AX629571 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6612 from Patent WO02053774.
ACCESSION AX629571
VERSION AX629571.1 GI:28457609
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6612 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCCT 20
||| |||||
Db 2 GCGCCTTCCT 11

RESULT 104

AX629791/c
LOCUS AX629791 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 6832 from Patent WO02053774.
ACCESSION AX629791
VERSION AX629791.1 GI:28457829
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6832 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CCTCATCGCC 13
||| |||||
Db 10 CCTCATCACC 1

RESULT 105
AX630124/c
LOCUS AX630124 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7165 from Patent WO02053774.
ACCESSION AX630124
VERSION AX630124.1 GI:28458162
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7165 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 73;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCTA 21
||| |||||
Db 10 CCCCATCCTA 1

RESULT 106
AX630572/c
LOCUS AX630572 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7613 from Patent WO02053774.
ACCESSION AX630572
VERSION AX630572.1 GI:28458610
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7613 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

FEATURES
source
1..11
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"


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CQ766296
LOCUS       CQ766296               12 bp    DNA
DEFINITION   Sequence 257 from Patent WO2004005547.
ACCESSION   CQ766296
VERSION      CQ766296.1 GI:44908556
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl, R.
METHOD       Method
JOURNAL      IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
    |||||
Db 3 CCACCTCAGC 12

RESULT 112
AR199106/c
LOCUS       AR199106               12 bp    DNA
DEFINITION   Sequence 54 from patent US 6355418.
ACCESSION   AR199106
VERSION      AR199106.1 GI:20249180
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Schmidt, G.
TITLE        Chimeric oligonucleotides and uses thereof in the identification of
            antisense binding sites
JOURNAL      Patent: US 6355418-A 54 12-MAR-2002;
FEATURES     source
            1..12
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CTTTCCTAAG 23
    |||||
Db 10 CTTTCCTAAG 1

RESULT 113
AR408041/c
LOCUS       AR408041               12 bp    RNA
DEFINITION   Sequence 134 from patent US 6632057.
ACCESSION   AR408041
VERSION      AR408041.1 GI:40158028
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Fauchet, C.R.J.
TITLE        Fixing unit with an end imprint in a threaded terminal portion
JOURNAL      Patent: US 6632057-A 134 14-OCT-2003;

CQ766296
LOCUS       CQ766296               12 bp    DNA
DEFINITION   Sequence 257 from Patent WO2004005547.
ACCESSION   CQ766296
VERSION      CQ766296.1 GI:44908556
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Weinzierl, R.
METHOD       Method
JOURNAL      IMPERIAL COLLEGE INNOVATIONS LIMITED (GB)
FEATURES     source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="HS motif"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
    |||||
Db 3 CCACCTCAGC 12

RESULT 112
AR199106/c
LOCUS       AR199106               12 bp    DNA
DEFINITION   Sequence 54 from patent US 6355418.
ACCESSION   AR199106
VERSION      AR199106.1 GI:20249180
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Schmidt, G.
TITLE        Chimeric oligonucleotides and uses thereof in the identification of
            antisense binding sites
JOURNAL      Patent: US 6355418-A 54 12-MAR-2002;
FEATURES     source
            1..12
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CTTTCCTAAG 23
    |||||
Db 10 CTTTCCTAAG 1

RESULT 113
AR408041/c
LOCUS       AR408041               12 bp    RNA
DEFINITION   Sequence 134 from patent US 6632057.
ACCESSION   AR408041
VERSION      AR408041.1 GI:40158028
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 12)
AUTHORS      Fauchet, C.R.J.
TITLE        Fixing unit with an end imprint in a threaded terminal portion
JOURNAL      Patent: US 6632057-A 134 14-OCT-2003;

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GFI Aerospace; Paris;
FRX; Location/Qualifiers
            1..12
            /organism="unknown"
            /mol_type="unassigned RNA"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTTCCTAAGC 24
    |||||
Db 12 CTTTCCTAGGC 3

RESULT 114
AX467018/c
LOCUS       AX467018               12 bp    DNA
DEFINITION   Sequence 47 from Patent WO0224950.
ACCESSION   AX467018
VERSION      AX467018.1 GI:21900359
KEYWORDS     .
SOURCE       synthetic construct
            other sequences; artificial sequences.
REFERENCE    1
AUTHORS      Liang, Z., Zhang, H.Y. and Wahlestedt, C.
TITLE        Methods and means of rna analysis
JOURNAL      Patent: WO 0224950-A 47 28-MAR-2002;
            Neuromics Inc. (US)
FEATURES     source
            1..12
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetically generated oligonucleotide"

Query Match      32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 80;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
    |||||
Db 12 CCACCGCATC 3

RESULT 115
AR121979
LOCUS       AR121979               10 bp    DNA
DEFINITION   Sequence 16 from patent US 6160202.
ACCESSION   AR121979
VERSION      AR121979.1 GI:14105555
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Bustos, M.M. and Chern, M.-S.
TITLE        Modification of seed crops with transcription factors
JOURNAL      Patent: US 6160202-A 16 12-DEC-2000;
FEATURES     source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
    |||||
Db 2 CCACCTCA 9

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RESULT 116
AR121983
LOCUS       AR121983
DEFINITION Sequence 20 from patent US 6160202.
ACCESSION  AR121983
VERSION     AR121983.1  GI:14105559
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Bustos,M.M. and Chern,M.-S.
TITLE       Modification of seed crops with transcription factors
JOURNAL    Patent: US 6160202-A 20 12-DEC-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches          8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTCA 8
        |||||
Db      2 CCACCTCA 9

RESULT 117
AR121984
LOCUS       AR121984
DEFINITION Sequence 21 from patent US 6160202.
ACCESSION  AR121984
VERSION     AR121984.1  GI:14105560
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Bustos,M.M. and Chern,M.-S.
TITLE       Modification of seed crops with transcription factors
JOURNAL    Patent: US 6160202-A 21 12-DEC-2000;
FEATURES   Location/Qualifiers
            source
            1..10
            /organism="unknown"
            /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches          8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTCA 8
        |||||
Db      2 CCACCTCA 9

RESULT 118
BD161336
LOCUS       BD161336
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION  BD161336
VERSION     BD161336.1  GI:27867094
KEYWORDS   JP 2002186482-A/158.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE       Human activated Th1 and Th2 cell expression genes

JOURNAL    Patent: JP 2002186482-A 158 02-JUL-2002;
            JAPAN SCIENCE AND TECHNOLOGY CORP
            OS Homo sapiens (human)
            PN JP 2002186482-A/158
            PD 02-JUL-2002
            PF 19-DEC-2000 JP 2000385816
            PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
            C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
            activated Th1 and Th2 cell expression genes FH Key
            Location/Qualifiers
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            1..10
            /organism='Homo sapiens (human)'.

FEATURES   source
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            Location/Qualifiers
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches          8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 CCCCTTC 19
        |||||
Db      3 CCCCTTC 10

RESULT 119
BD239260/c
LOCUS       BD239260
DEFINITION Preparation and use of superior vaccines.
ACCESSION  BD239260
VERSION     BD239260.1  GI:33049030
KEYWORDS   JP 2002534056-A/678.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1 (bases 1 to 10)
AUTHORS    Roberts,B.L. and Shankara,S.
TITLE       Preparation and use of superior vaccines
JOURNAL    Patent: JP 2002534056-A 678 15-OCT-2002;
            GENZYME CORP
            OS Homo sapiens (human)
            PN JP 2002534056-A/678
            PD 15-OCT-2002
            PF 18-JUN-1999 JP 2000554749
            PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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            08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
            19-JUN-1998 US 60/111715
            PI BRUCE L ROBERTS,SRINIVAS SHANKARA
            PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
            C12N1/19,
            PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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QY 12 CCCCTTCC 19
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Db 8 CCCCTTCC 1

RESULT 120
BD239623/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 10)
    Roberts,B.L. and Shankara,S.
    Preparation and use of superior vaccines
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    JOURNAL
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    PN JP 2002534056-A/1041
    PD 15-OCT-2002
    PF 18-JUN-1999 JP 2000554749
    PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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    08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
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DEFINITION
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VERSION
KEYWORDS
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    Homnidae; Homo.
REFERENCE
    1 (bases 1 to 10)
    Roberts,B.L. and Shankara,S.
    Preparation and use of superior vaccines
    TITLE
    JOURNAL
    GENZYME CORP
    OS Homo sapiens (human)
    PN JP 2002534056-A/1076
    PD 15-OCT-2002
    PF 18-JUN-1999 JP 2000554749
    PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
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    19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
    19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
    19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
    19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
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    08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
    08-DEC-1998 US 60/111715
    PI BRUCE L ROBERTS, SRINIVAS SHANKARA
    PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
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Homnidae; Homo.
REFERENCE
AUTHORS  Roberts,B.I. and Shankara,S.
TITLE    Preparation and use of superior vaccines
JOURNAL  Patent: JP 2002534056-A 1437 15-OCT-2002;
GENZYME CORP
COMMENT  OS Homo sapiens (human)
PN JP 2002534056-A/1437
PD 15-OCT-2002
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PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCACCTCA 8
Db 3 CCACCTCA 10
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LOCUS Oligonucleotides of lettuce's DNA for primer.
DEFINITION Oligonucleotides of lettuce's DNA for primer.
ACCESSION E07298
VERSION E07298.1 GI:2175439
KEYWORDS JP 1994113849-A/1.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE
AUTHORS Yamamoto,T. and Nishikawa,A.
TITLE METHOD FOR DISTINGUISHING VARIETY OF LETTUCE USING OLIGONUCLEOTIDE
AND ITS OLIGONUCLEOTIDE
JOURNAL Patent: JP 1994113849-A 1 26-APR-1994;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994113849-A/1
PD 26-APR-1994
PF 09-OCT-1992 JP 1992271759
PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/53;
CC strandedness: Single;
CC topology: Linear;
CC anti-sense: No; Location/Qualifiers
FH Key
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Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 17 TCCTAAGC 24
Db 3 TCCTAAGC 10
RESULT 125
E07298
LOCUS Oligonucleotide of rice plant's DNA for primer.
DEFINITION Oligonucleotide of rice plant's DNA for primer.
ACCESSION E07306
VERSION E07306.1 GI:2175447
KEYWORDS JP 1994113850-A/1.
SOURCE unidentifed
ORGANISM unclassified.
REFERENCE
AUTHORS Yamamoto,T. and Nishikawa,A.
TITLE METHOD FOR DISTINGUISHING VARIETY OF RICE PLANT USING
OLIGONUCLEOTIDE AND ITS OLIGONUCLEOTIDE
JOURNAL Patent: JP 1994113850-A 1 26-APR-1994;
SUMITOMO CHEM CO LTD
COMMENT OS None
OC Artificial sequences.
PN JP 1994113850-A/1
PD 26-APR-1994
PF 09-OCT-1992 JP 1992271760
PI YAMAMOTO TOSHIYA, NISHIKAWA AKIRA
PC C12N15/11,C12Q1/68,G01N33/48,G01N33/53;
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CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No; Location/Qualifiers
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Db 3 TCCTAAGC 10
RESULT 125
E39656/c
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LOCUS       E39656                               10 bp    DNA    linear    PAT 31-JAN-2002
DEFINITION   Genes with human dendritic cell expression.
ACCESSION    E39656
VERSION      E39656.1 GI:18621747
KEYWORDS     JP 2000279181-A/189,
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 10)
AUTHORS      Hashimoto,S., Matsushima,K. and Suzuki,T.
TITLE        Genes with human dendritic cell expression
JOURNAL      Patent: JP 2000279181-A 189 10-OCT-2000;
              SCIENCE & TECH AGENCY
COMMENT      OS Homo sapiens (human)
              PN JP 2000279181-A/189
              PD 10-OCT-2000
              PF 01-APR-1999 JP 1999095481
              PR
              PI SHINICHI HASHIMOTO,KOJI MATSUSHIMA,TAKUJI SUZUKI PC
              CC C12N15/09,C07K14/475,C07K16/18,C12N15/00
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCC 19
Db 8 CCCCTTCC 1

RESULT 126
AR561756/c
LOCUS       AR561756                               10 bp    DNA    linear    PAT 08-OCT-2004
DEFINITION   Sequence 20 from patent US 6759195.
ACCESSION    AR561756
VERSION      AR561756.1 GI:53975407
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Bentley,W.E. and Gill,R.
TITLE        Method of differential display of prokaryotic messenger RNA by
              RT-PCR
JOURNAL      Patent: US 6759195-A 20 06-JUL-2004;
              University of Maryland Biotechnology Institute; Baltimore, MD
FEATURES     source
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QY 6 TCATCGCC 13
Db 10 TCATCGCC 3

RESULT 127
AR575231
LOCUS       AR575231                               10 bp    DNA    linear    PAT 31-JAN-2002
DEFINITION   LPS activated human monocyte expressing genes.
ACCESSION    BD007786
VERSION      BD007786.1 GI:18636159
KEYWORDS     JP 2001069993-A/62.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 10)

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LOCUS       AR575231                               10 bp    DNA    linear    PAT 14-DEC-2004
DEFINITION   Sequence 69 from patent US 6770738.
ACCESSION    AR575231
VERSION      AR575231.1 GI:56576127
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unknown.
REFERENCE    1 (bases 1 to 10)
AUTHORS      Ecker,D.J., Buchardt,O., Egholm,M., Nielsen,P.E., Berg,R.H. and
              Mollegaard,N.E.
TITLE        Higher order structure and binding of peptide nucleic acids
JOURNAL      Patent: US 6770738-A 69 03-AUG-2004;
              ISIS Pharmaceuticals, Inc.; Carlsbad, CA
FEATURES     Location/Qualifiers
              source
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Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 128
AX467563
LOCUS       AX467563                               10 bp    DNA    linear    PAT 16-JUL-2002
DEFINITION   Sequence 2 from Patent WO0218607.
ACCESSION    AX467563
VERSION      AX467563.1 GI:21900758
KEYWORDS     .
SOURCE       synthetic construct
              other sequences; artificial sequences.
ORGANISM     1
REFERENCE    1
AUTHORS      Conkling,M.A. and Li,Y.
TITLE        Transgenic plants containing molecular decoys that alter protein
              content therein
JOURNAL      Patent: WO 0218607-A 2 07-MAR-2002;
              NORTH CAROLINA STATE UNIVERSITY (US)
FEATURES     Location/Qualifiers
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Query Match      30.8%; Score 8; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
Db 2 CCACCTCA 9

RESULT 129
BD007786/c
LOCUS       BD007786                               10 bp    DNA    linear    PAT 31-JAN-2002
DEFINITION   LPS activated human monocyte expressing genes.
ACCESSION    BD007786
VERSION      BD007786.1 GI:18636159
KEYWORDS     JP 2001069993-A/62.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 10)

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AUTHORS Matsushima,K., Hashimoto,S. and Suzuki,T.
 TITLE LPS activated human monocyte expressing genes
 JOURNAL Patent: JP 2001069993-A 62 21-MAR-2001;
 JAPAN SCIENCE AND TECHNOLOGY CORP
 COMMENT OS Homo sapiens (human)
 PN JP 2001069993-A/62
 PD 21-MAR-2001
 PF 28-APR-2000 JP 2000131079
 PR KOJI MATSUSHIMA,SHINICHI HASHIMOTO,TAKUJI SUZUKI PC
 P1 C12N15/09,C07K14/47,C07K16/18,G01N33/50,G01N33/53//A61K45/00, PC
 A61P29/00,
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 QY 12 CCCCTTCC 19
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 Db 9 CCCCTTCC 2
 RESULT 130
 A15322
 LOCUS
 DEFINITION Oligonucleotide C48.
 ACCESSION A15322
 VERSION A15322.1 GI:512136
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences: artificial sequences.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
 TITLE A process for the production of alpha-human atrial natriuretic polypeptide
 JOURNAL Patent: EP 0206769-A 61 30-DEC-1986;
 FUJISAWA PHARMACEUTICAL CO., LTD
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 Db 4 TCATCGCC 11
 RESULT 131
 A16522
 LOCUS
 DEFINITION Oligonucleotide C48.
 ACCESSION A16522
 VERSION A16522.1 GI:489910
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 other sequences: artificial sequences.

REFERENCE 1 (bases 1 to 11)
 AUTHORS Ueda,I., Niwa,M., Saito,Y., Yamada,H. and Ishii,Y.
 TITLE A process for the production of alpha-human atrial natriuretic polypeptide
 JOURNAL Patent: EP 0440311-A 78 07-AUG-1991;
 FUJISAWA PHARMACEUTICAL CO., LTD
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 QY 6 TCATCGCC 13
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 Db 4 TCATCGCC 11
 RESULT 132
 AR004550
 LOCUS
 DEFINITION Sequence 9 from patent US 5747253.
 ACCESSION AR004550
 VERSION AR004550.1 GI:3965429
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Ecker,D.J., Vickers,T. and Davis,P.
 TITLE Combinatorial oligomer immunoabsorbant screening assay for transcription factors and other biomolecule binding
 JOURNAL Patent: US 5747253-A 9 05-MAY-1998;
 FEATURES
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 /mol_type="unassigned DNA"
 Query Match 30.8%; Score 8; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 CCCTTCCT 20
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 Db 1 CCCTTCCT 8
 RESULT 133
 AR032093
 LOCUS
 DEFINITION Sequence 14 from patent US 5866698.
 ACCESSION AR032093
 VERSION AR032093.1 GI:5946382
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 11)
 AUTHORS Ecker,D., Vickers,T.A. and Bruice,T.W.
 TITLE Modulation of gene expression through interference with RNA secondary structure
 JOURNAL Patent: US 5866698-A 14 02-FEB-1999;
 FEATURES
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Qy 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 134
CQ828745
LOCUS CQ828745 11 bp DNA linear PAT 05-JUL-2004
DEFINITION Sequence 463 from Patent WO2004053120.
ACCESSION CQ828745
VERSION CQ828745.1 GI:49732228
KEYWORDS Mus musculus (house mouse)
SOURCE
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidae; Muridae; Mus.

REFERENCE 1
AUTHORS Weihe, E., Bieller, A. and Schaefer, M. K.
TITLE Regulatory elements in the 5' region of the vrl gene
JOURNAL Patent: WO 2004053120-A 463 24-JUN-2004;
Gruenenthal GmbH (DE)
FEATURES Location/Qualifiers
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/note="V\$DELTAEBF1 01"

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCAT 9
Db 4 CACCTCAT 11

RESULT 135
CQ833719
LOCUS CQ833719 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 1090 from Patent WO2004059002.
ACCESSION CQ833719
VERSION CQ833719.1 GI:50833326
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
CONRADT, M. and Hofmann, K.
TITLE Method for determining the homeostasis of hairy skin
JOURNAL Patent: WO 2004059002-A 1090 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 TTCCTAAG 23
Db 4 TTCCTAAG 11

RESULT 136

CQ835404/c
LOCUS CQ835404 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 462 from Patent WO2004059001.
ACCESSION CQ835404
VERSION CQ835404.1 GI:50834938
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
CONRADT, M. and Hofmann, K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 462 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTCA 8
Db 10 CCACCTCA 3

RESULT 137
CQ835452
LOCUS CQ835452 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 510 from Patent WO2004059001.
ACCESSION CQ835452
VERSION CQ835452.1 GI:50834986
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Petersohn, D., Schlotmann, K., Gassenmeier, T., Holtkoetter, O.,
CONRADT, M. and Hofmann, K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 510 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES Location/Qualifiers
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCT 20
Db 3 CCCTTCCT 10

RESULT 138
CQ837286/c
LOCUS CQ837286 11 bp DNA linear PAT 29-JUL-2004
DEFINITION Sequence 2344 from Patent WO2004059001.
ACCESSION CQ837286
VERSION CQ837286.1 GI:50836820
KEYWORDS Homo sapiens (human)
SOURCE

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2344 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCCCTT 17
Db 8 CGCCCCCTT 1

RESULT 139
CQ837568
LOCUS Sequence 2626 from Patent WO2004059001.
DEFINITION
ACCESSION CQ837568
VERSION CQ837568.1 GI:50837102
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 2626 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCTCTAA 22
Db 3 CTTCTCTAA 10

RESULT 140
CQ838068
LOCUS Sequence 3126 from Patent WO2004059001.
DEFINITION
ACCESSION CQ838068
VERSION CQ838068.1 GI:50837602
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.

```

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TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3126 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CCTTCCTA 21
Db 2 CCTTCCTA 9

RESULT 141
CQ838137/c
LOCUS Sequence 3195 from Patent WO2004059001.
DEFINITION
ACCESSION CQ838137
VERSION CQ838137.1 GI:50837671
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
Conradt,M. and Hofmann,K.
TITLE Method for determining markers of human facial skin
JOURNAL Patent: WO 2004059001-A 3195 15-JUL-2004;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCAT 9
Db 9 CACCTCAT 2

RESULT 142
CS058235
LOCUS Sequence 132 from Patent WO2005028671.
DEFINITION
ACCESSION CS058235
VERSION CS058235.1 GI:62551418
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Holtkoetter,O., Petersohn,D., Schlotmann,K., Giesen,M. and
Kessler-Becker,D.
TITLE Method for determining hair cycle markers
JOURNAL Patent: WO 2005028671-A 132 31-MAR-2005;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"

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/db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ATCGCCCC 15
Db 4 ATCGCCCC 11

RESULT 143
LOCUS      I67665
DEFINITION Sequence 9 from patent US 5672472.
ACCESSION  I67665
VERSION     I67665.1 GI:2731200
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Ecker,D.J., Wyatt,J., Bruice,T.W., Anderson,K., Hanecak,R.C.,
            Vickers,T. and Davis,P.
TITLE       Synthetic unrandomization of oligomer fragments
JOURNAL     Patent: US 5672472-A 9 30-SEP-1997;
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 144
LOCUS      I85557
DEFINITION Sequence 9 from patent US 5698391.
ACCESSION  I85557
VERSION     I85557.1 GI:3205275
KEYWORDS    Unknown.
SOURCE      Unknown.
ORGANISM    Unclassified.
REFERENCE   1 (bases 1 to 11)
AUTHORS     Cook,P.Dan., Ecker,D.J., Wyatt,J., Bruice,T.W., Anderson,K.,
            Hanecak,R., Vickers,T., Davis,P., Freier,S.M., Sanghvi,Y.S. and
            Brown-Driver,V.
TITLE       Methods for synthetic unrandomization of oligomer fragments
JOURNAL     Patent: US 5698391-A 9 16-DEC-1997;
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="unknown"
                /mol_type="unassigned DNA"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 CCCTTCCT 20
Db 1 CCCTTCCT 8

RESULT 145
AX471421/c
LOCUS      AX471421
DEFINITION Sequence 998 from Patent WO02053773.
ACCESSION  AX471421
VERSION     AX471421.1 GI:22206546
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 998 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TCCTAAGC 24
Db 11 TCCTAAGC 4

RESULT 146
AX471761
LOCUS      AX471761
DEFINITION Sequence 1338 from Patent WO02053773.
ACCESSION  AX471761
VERSION     AX471761.1 GI:22206886
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE   1
AUTHORS     Hofmann,K., Conradt,M. and Petersohn,D.
TITLE       Method for determining skin stress or skin ageing in vitro
JOURNAL     Patent: WO 02053773-A 1338 11-JUL-2002;
            HENKEL KGAA (DE)
FEATURES    Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTCC 19
Db 4 CCCCTTCC 11

RESULT 147
AX623532/c
LOCUS      AX623532
DEFINITION Sequence 573 from Patent WO02053774.
ACCESSION  AX623532
VERSION     AX623532.1 GI:28451473
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.

```

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REFERENCE
1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 573 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCAT 9
Db 9 CACCTCAT 2

RESULT 148
AX623940/c
LOCUS      AX623940
DEFINITION Sequence 981 from Patent WO02053774.
ACCESSION  AX623940
VERSION     AX623940.1 GI:28451881
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 981 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCTT 17
Db 8 CGCCCTT 1

RESULT 149
AX624535
LOCUS      AX624535
DEFINITION Sequence 1576 from Patent WO02053774.
ACCESSION  AX624535
VERSION     AX624535.1 GI:28452476
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1576 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCCTAA 22
Db 3 CTTCCTAA 10
```

```
REFERENCE
1
AUTHORS      Petersohn,D., Conradt,M. and Hofmann,K.
TITLE        Method for determining homeostasis of the skin
JOURNAL      Patent: WO 02053774-A 573 11-JUL-2002;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ATCGCCCC 15
Db 4 ATCGCCCC 11

RESULT 150
AX624841/c
LOCUS      AX624841
DEFINITION Sequence 1882 from Patent WO02053774.
ACCESSION  AX624841
VERSION     AX624841.1 GI:28452782
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 1882 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
Db 11 TCCTAAGC 4

RESULT 151
AX626013
LOCUS      AX626013
DEFINITION Sequence 3054 from Patent WO02053774.
ACCESSION  AX626013
VERSION     AX626013.1 GI:28454051
KEYWORDS   .
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1
AUTHORS    Petersohn,D., Conradt,M. and Hofmann,K.
TITLE      Method for determining homeostasis of the skin
JOURNAL    Patent: WO 02053774-A 3054 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
   /organism="Homo sapiens"
   /mol_type="unassigned DNA"
   /db_xref="taxon:9606"

Query Match
Best Local Similarity 30.8%; Score 8; DB 1; Length 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCCTAA 22
Db 3 CTTCCTAA 10
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RESULT 152
AX626608
LOCUS      AX626608      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3649 from Patent WO02053774.
ACCESSION  AX626608
VERSION     AX626608.1  GI:28454646
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3649 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13  CCCTTCCT 20
Db      3  CCCTTCCT 10

RESULT 153
AX628205/c
LOCUS      AX628205      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5246 from Patent WO02053774.
ACCESSION  AX628205
VERSION     AX628205.1  GI:28456243
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5246 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14  CCTTCCTA 21
Db      11  CCTTCCTA 4

RESULT 154
AX628339
LOCUS      AX628339      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 5380 from Patent WO02053774.
ACCESSION  AX628339
VERSION     AX628339.1  GI:28456377
KEYWORDS

```

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SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 5380 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CCACCTCA 8
Db      4  CCACCTCA 11

RESULT 155
AX629051
LOCUS      AX629051      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 6092 from Patent WO02053774.
ACCESSION  AX629051
VERSION     AX629051.1  GI:28457089
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 6092 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source      1..11
            /organism="Homo sapiens"
            /mol_type="unassigned DNA"
            /db_xref="taxon:9606"
Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14  CCTTCCTA 21
Db      2  CCTTCCTA 9

RESULT 156
AX630007
LOCUS      AX630007      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 7048 from Patent WO02053774.
ACCESSION  AX630007
VERSION     AX630007.1  GI:28458045
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominoidea; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 7048 11-JUL-2002;

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          /mol_type="unassigned DNA"
          /db_xref="taxon:9606"

Query Match
  30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 GCCCTTC 18
Db 4 GCCCTTC 11

RESULT 157
AX630953/c
LOCUS
  AX630953
DEFINITION
  Sequence 7994 from Patent WO02053774.
ACCESSION
  AX630953
VERSION
  AX630953.1 GI:28458995
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 7994 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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QY 2 CACCTCAT 9
Db 9 CACCTCAT 2

RESULT 158
AX631361/c
LOCUS
  AX631361
DEFINITION
  Sequence 8403 from Patent WO02053774.
ACCESSION
  AX631361
VERSION
  AX631361.1 GI:28459407
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 8403 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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      /mol_type="unassigned DNA"
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    Best Local Similarity 100.0%; Pred. No. 88;

QY 17 TCCTAAGC 24
Db 11 TCCTAAGC 4

RESULT 161
AR024154

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Best Local Similarity 100.0%; Pred. No. 88;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 CGCCCTT 17
Db 8 CGCCCTT 1

RESULT 159
AX631956
LOCUS
  AX631956
DEFINITION
  Sequence 8998 from Patent WO02053774.
ACCESSION
  AX631956
VERSION
  AX631956.1 GI:28467571
KEYWORDS
  .
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 8998 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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      /db_xref="taxon:9606"

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QY 8 ATCGCCCC 15
Db 4 ATCGCCCC 11

RESULT 160
AX632262/c
LOCUS
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DEFINITION
  Sequence 9304 from Patent WO02053774.
ACCESSION
  AX632262
VERSION
  AX632262.1 GI:28467877
KEYWORDS
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SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominidae; Homo.
REFERENCE
  1
  Petersohn,D., Conradt,M. and Hofmann,K.
  Method for determining homeostasis of the skin
  Patent: WO 02053774-A 9304 11-JUL-2002;
  Henkel Kommanditgesellschaft auf Aktien (DE)
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      /mol_type="unassigned DNA"
      /db_xref="taxon:9606"

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    Best Local Similarity 100.0%; Pred. No. 88;
    Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TCCTAAGC 24
Db 11 TCCTAAGC 4

RESULT 161
AR024154

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LOCUS       AR024154                      11 bp    DNA          linear      PAT 05-DEC-1998
DEFINITION   Sequence 104 from patent US 5795778.
ACCESSION    AR024154
VERSION      AR024154.1 GI:3977448
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Draper,K.G.
TITLE        Method and reagent for inhibiting herpes simplex virus replication
JOURNAL      Patent: US 5795778-A 104 18-AUG-1998;
FEATURES     Location/Qualifiers
             source
               1..11
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
   |||||
Db 1 CCCCTTCCT 11

RESULT 162
LOCUS       AR030166                      11 bp    DNA          linear      PAT 29-SEP-1999
DEFINITION   Sequence 355 from patent US 5861244.
ACCESSION    AR030166
VERSION      AR030166.1 GI:5943380
KEYWORDS     .
SOURCE       Unknown.
ORGANISM     Unclassified.
REFERENCE    1 (bases 1 to 11)
AUTHORS      Wang,C.-G. and Hepburn,A.G.
TITLE        Genetic sequence assay using DNA triple strand formation
JOURNAL      Patent: US 5861244-A 355 19-JAN-1999;
FEATURES     Location/Qualifiers
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               1..11
               /organism="unknown"
               /mol_type="unassigned DNA"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
   |||||
Db 1 CTCCTTCCTCC 11

RESULT 163
LOCUS       BD124409/c                    11 bp    DNA          linear      PAT 18-SEP-2002
DEFINITION   Compositions and method for healing wound.
ACCESSION    BD124409
VERSION      BD124409.1 GI:23219354
KEYWORDS     JP 2002503460-A/240.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
REFERENCE    1 (bases 1 to 11)
AUTHORS      Katz,E.H.
TITLE        Compositions and method for healing wound
JOURNAL      Patent: JP 2002503460-A 240 05-FEB-2002;
COMMENT      THE WISTAR INSTITUTE
             OS Mus musculus (mouse)
             PN JP 2002503460-A/240

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PD 05-FEB-2002
PF 12-FEB-1999 JP 2000531545
PR 13-FEB-1998 US 60/074737,26-AUG-1998 US 60/097937 PR
28-SEP-1998 US 60/102051
PI ELLEN HEBER KATZ
PC C12N15/09,A01K67/027,C12N5/10,C12Q1/68,G01N33/50,C12N15/00, PC
C12N5/00
CC Compositions and method for healing wound
FH Key 1..11 Location/Qualifiers
FT source
   1..11
   Location/Qualifiers
   1..11
   /organism="Mus musculus"
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   /db_xref="taxon:10090"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTCCTAAGCA 25
   |||||
Db 11 CATCATAGCA 1

RESULT 164
LOCUS       CQ832668                      11 bp    DNA          linear      PAT 29-JUL-2004
DEFINITION   Sequence 39 from Patent WO2004059002.
ACCESSION    CQ832668
VERSION      CQ832668.1 GI:50832275
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Conradt,M. and Hofmann,K.
TITLE        Method for determining the homeostasis of hairy skin
JOURNAL      Patent: WO 2004059002-A 39 15-JUL-2004;
              Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES     Location/Qualifiers
             source
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               /mol_type="unassigned DNA"
               /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
   |||||
Db 1 CCCCCACCTAA 11

RESULT 165
LOCUS       CQ833592                      11 bp    DNA          linear      PAT 29-JUL-2004
DEFINITION   Sequence 963 from Patent WO2004059002.
ACCESSION    CQ833592
VERSION      CQ833592.1 GI:50833199
KEYWORDS     .
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1
AUTHORS      Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Homnidae; Homo.

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QY      10 CGCCCTTCTCT 20
Db      1 CGCCGCTTCT 11

RESULT 170
LOCUS   CQ838066/c
DEFINITION Sequence 3124 from Patent WO2004059001.
ACCESSION CQ838066
VERSION   CQ838066.1 GI:50837600
KEYWORDS Homo sapiens (human)
SOURCE   Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS  Petersohn,D., Schlotmann,K., Gassenmeier,T., Holtkoetter,O.,
          Conradt,M. and Hofmann,K.
TITLE    Method for determining markers of human facial skin
JOURNAL  Patent: WO 2004059001-A 3124 15-JUL-2004;
          Henkel Kommanditgesellschaft auf Aktien (DE)
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source   1..11
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/db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 TCATCGCCCT 16
Db      11 TCTGCGCCCT 1

RESULT 171
LOCUS   CS086765/c
DEFINITION Sequence 14 from Patent WO2005042018.
ACCESSION CS086765
VERSION   CS086765.1 GI:66712216
KEYWORDS synthetic construct
SOURCE   synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS  Uhlmann,E., Vollmer,J., Krieg,A.M. and Noll,B.O.
TITLE    C-class oligonucleotide analogs with enhanced immunostimulatory
          potency
JOURNAL  Patent: WO 2005042018-A 14 12-MAY-2005;
          Coley Pharmaceutical GmbH (DE); Coley Pharmaceutical Group, Inc.
          (US)
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source      Location/Qualifiers
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/mol_type="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      3 ACCTCATCGCC 13
Db      11 ACCTCTCGAC 1

RESULT 172
LOCUS   AR224372
DEFINITION Sequence 104 from patent US 6440719.
ACCESSION AR224372
VERSION   AR224372.1 GI:23333149
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS  Draper,K.G.
TITLE    Method and reagent for inhibiting herpes simplex virus replication
JOURNAL  Patent: US 6440719-A 104 27-AUG-2002;
          Ribozyme Pharmaceuticals, Inc.; Boulder, CO
FEATURES
source      Location/Qualifiers
1..11
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCT 20
Db      1 CGCCCTTCTCT 11

RESULT 173
LOCUS   AR301659/c
DEFINITION Sequence 240 from patent US 6538173.
ACCESSION AR301659
VERSION   AR301659.1 GI:31689461
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS  Heber-Katz,E.
TITLE    Compositions and methods for wound healing
JOURNAL  Patent: US 6538173-A 240 25-MAR-2003;
          The Wistar Institute; Philadelphia, PA;
          WOX;
FEATURES
source      Location/Qualifiers
1..11
/mol_type="unknown"
/mol_type="genomic DNA"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      15 CTTCTTAAGCA 25
Db      11 CATCATAAGCA 1

RESULT 174
LOCUS   AR365391/c
DEFINITION Sequence 21 from patent US 5494663.
ACCESSION AR365391
VERSION   AR365391.1 GI:34428970
KEYWORDS Unknown.
SOURCE   Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 11)
AUTHORS  Yamada,M., Furutani,Y., Yamayoshi,M., Notake,M. and Yamagishi,J.
TITLE    Treatment of microbial infection with interleukin 1 polypeptides
JOURNAL  Patent: US 5494663-A 21 27-FEB-1996;
          Daiippon Pharmaceutical Co., Ltd.; Osaka;
          JPX;

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[illegible]

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ACCESSION AX624516
VERSION AX624516.1 GI:28452457
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1557 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTCATGCG 12
|||||
Db 1 CACCCCTCGC 11

RESULT 180
AX624591/c
LOCUS AX624591 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1632 from Patent WO02053774.
ACCESSION AX624591
VERSION AX624591.1 GI:28452532
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1632 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
/organism="Homo sapiens"
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/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTCAAGCA 25
|||||
Db 11 CTTCCGACGA 1

RESULT 181
AX624873/c
LOCUS AX624873 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 1914 from Patent WO02053774.
ACCESSION AX624873
VERSION AX624873.1 GI:28452814
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
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AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 1914 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
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/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATCGCCCTTC 18
|||||
Db 11 AGCACCCCTTC 1

RESULT 182
AX625228
LOCUS AX625228 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2269 from Patent WO02053774.
ACCESSION AX625228
VERSION AX625228.1 GI:28453169
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2269 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
|||||
Db 1 CCCCCACCTAA 11

RESULT 183
AX625386
LOCUS AX625386 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 2427 from Patent WO02053774.
ACCESSION AX625386
VERSION AX625386.1 GI:28453327
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 2427 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CTCATCGCCCC 15
Db 1 CTCACCCCCC 11

RESULT 184
AX625728/c
LOCUS      AX625728      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 2769 from Patent WO02053774.
ACCESSION  AX625728
VERSION     AX625728.1 GI:28453669
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 2769 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19
Db 11 TCGACCTGCC 1

RESULT 185
AX625963/c
LOCUS      AX625963      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3004 from Patent WO02053774.
ACCESSION  AX625963
VERSION     AX625963.1 GI:28454001
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3004 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 TCGCCCTTCC 19
Db 11 TCGACCTGCC 1

RESULT 186
AX626384/c
LOCUS      AX626384      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 3425 from Patent WO02053774.
ACCESSION  AX626384
VERSION     AX626384.1 GI:28454422
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 3425 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCACCTCATCG 11
Db 11 CCTCTCGTCG 1

RESULT 187
AX627272/c
LOCUS      AX627272      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4313 from Patent WO02053774.
ACCESSION  AX627272
VERSION     AX627272.1 GI:28455310
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.
REFERENCE   1
AUTHORS     Petersohn,D., Conradt,M. and Hofmann,K.
TITLE       Method for determining homeostasis of the skin
JOURNAL     Patent: WO 02053774-A 4313 11-JUL-2002;
            Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES    Location/Qualifiers
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            1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 16 TTCTTAAGCAT 26
Db 11 TTCTCAGCCT 1

RESULT 188
AX627387/c
LOCUS      AX627387      11 bp      DNA      linear      PAT 21-FEB-2003
DEFINITION Sequence 4428 from Patent WO02053774.
ACCESSION  AX627387
VERSION     AX627387.1 GI:28455425
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homnidae; Homo.

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4428 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CCTCATCGCCC 14
Db 1 CCTCATTTCCC 11

RESULT 189
AX627599/c
LOCUS AX627599 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 4640 from Patent WO02053774.
ACCESSION AX627599
VERSION AX627599.1 GI:28455637
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 4640 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CCCCTTCCTAA 22
Db 11 CTCCTCCCTAA 1

RESULT 190
AX628049
LOCUS AX628049 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5090 from Patent WO02053774.
ACCESSION AX628049
VERSION AX628049.1 GI:28456087
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5090 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)

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FEATURES
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1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 CCCCTTCCTAA 22
Db 1 CCCCTTCCTTA 11

RESULT 191
AX628099/c
LOCUS AX628099 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5140 from Patent WO02053774.
ACCESSION AX628099
VERSION AX628099.1 GI:28456137
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5140 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TCATCGCCCTC 16
Db 11 TCCTCTCCCT 1

RESULT 192
AX628377/c
LOCUS AX628377 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5418 from Patent WO02053774.
ACCESSION AX628377
VERSION AX628377.1 GI:28456415
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5418 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 TCATCGCCCTC 16
Db 11 TCCTCTCCCT 1

RESULT 192
AX628377/c
LOCUS AX628377 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 5418 from Patent WO02053774.
ACCESSION AX628377
VERSION AX628377.1 GI:28456415
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 5418 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1. .11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      6 TCATCGCCCT 16
Db      11 TCTGCGCCCT 1

RESULT 193
LOCUS   AX628495/c
DEFINITION Sequence 5536 from Patent WO02053774.
ACCESSION AX628495
VERSION   AX628495.1 GI:28456533
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 5536 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      14 CCTTCCTAAGC 24
Db      11 CCTTCCTCGGC 1

RESULT 196
LOCUS   AX629429/c
DEFINITION Sequence 6470 from Patent WO02053774.
ACCESSION AX629429
VERSION   AX629429.1 GI:28457467
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 6470 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CACCTCATCGC 12
Db      11 CGCCTCGTCGC 1

RESULT 197
LOCUS   AX629767/c
DEFINITION Sequence 6808 from Patent WO02053774.
ACCESSION AX629767
VERSION   AX629767.1 GI:28457805
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

QY      6 TCATCGCCCT 16
Db      11 TCTGCGCCCT 1

RESULT 193
LOCUS   AX628495/c
DEFINITION Sequence 5536 from Patent WO02053774.
ACCESSION AX628495
VERSION   AX628495.1 GI:28456533
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 5536 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
            source
              1..11
                /organism="Homo sapiens"
                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 CTCATCGCCCT 15
Db      11 CTGATCGCCTC 1

RESULT 194
LOCUS   AX629144
DEFINITION Sequence 6185 from Patent WO02053774.
ACCESSION AX629144
VERSION   AX629144.1 GI:28457182
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

REFERENCE 1
AUTHORS  Petersohn,D., Conradt,M. and Hofmann,K.
TITLE    Method for determining homeostasis of the skin
JOURNAL  Patent: WO 02053774-A 6185 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES  Location/Qualifiers
            source
              1..11
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                /mol_type="unassigned DNA"
                /db_xref="taxon:9606"

Query Match      30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches          9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 CGCCCTTCTCT 20
Db      1 CGCCGCTTCTT 11

RESULT 195
LOCUS   AX629301/c
DEFINITION Sequence 6808 from Patent WO02053774.
ACCESSION AX629301
VERSION   AX629301.1 GI:28457805
KEYWORDS .
SOURCE   Homo sapiens (human)
ORGANISM Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
          Hominiidae; Homo.

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REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 6808 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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  1. .11
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    /db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
Db 11 CCCCTTCCTAA 1

RESULT 198
AX630305/c
LOCUS AX630305 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7346 from Patent WO02053774.
ACCESSION AX630305
VERSION AX630305.1 GI:28458343
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7346 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  Location/Qualifiers
  1. .11
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    /mol_type="unassigned DNA"
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Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 ACCTCATCGCC 13
Db 11 ACCCATCGCC 1

RESULT 199
AX630373/c
LOCUS AX630373 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7414 from Patent WO02053774.
ACCESSION AX630373
VERSION AX630373.1 GI:28458411
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7414 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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    /mol_type="unassigned DNA"
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Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TCATCGCCCT 16
Db 1 TCAGCGACCT 11

RESULT 201
AX631451
LOCUS AX631451 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8493 from Patent WO02053774.
ACCESSION AX631451
VERSION AX631451.1 GI:28459517
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8493 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
  Location/Qualifiers
  1. .11
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAG 23
Db 1 CCTTACCTAAG 11

RESULT 200
AX630651
LOCUS AX630651 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 7692 from Patent WO02053774.
ACCESSION AX630651
VERSION AX630651.1 GI:28458689
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 7692 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
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  1. .11
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCC 14
Db 11 CCACAGCGCC 1

RESULT 201
AX631451
LOCUS AX631451 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8493 from Patent WO02053774.
ACCESSION AX631451
VERSION AX631451.1 GI:28459517
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8493 11-JUL-2002;
          Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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  Location/Qualifiers
  1. .11
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    /mol_type="unassigned DNA"
    /db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 CCCTTCCTAAG 23
Db 1 CCTTACCTAAG 11

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RESULT 202
AX631937
LOCUS AX631937 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 8979 from Patent WO02053774.
ACCESSION AX631937
VERSION AX631937.1 GI:28467552
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 8979 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CACCTCATCGC 12
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Db 1 CACCCCTCGC 11

RESULT 203
AX632012/c
LOCUS AX632012 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9054 from Patent WO02053774.
ACCESSION AX632012
VERSION AX632012.1 GI:28467627
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9054 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
source
1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTTAGCA 25
|||||
Db 11 CTTCCGACGA 1

RESULT 204
AX632294/c
LOCUS AX632294 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9336 from Patent WO02053774.
ACCESSION AX632294
VERSION AX632294.1 GI:28467909
KEYWORDS

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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9336 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ATCGCCCTTC 18
|||||
Db 11 AGCACCCCTTC 1

RESULT 205
AX632649
LOCUS AX632649 11 bp DNA linear PAT 21-FEB-2003
DEFINITION Sequence 9691 from Patent WO02053774.
ACCESSION AX632649
VERSION AX632649.1 GI:28468264
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1
REFERENCE
AUTHORS Petersohn,D., Conradt,M. and Hofmann,K.
TITLE Method for determining homeostasis of the skin
JOURNAL Patent: WO 02053774-A 9691 11-JUL-2002;
Henkel Kommanditgesellschaft auf Aktien (DE)
FEATURES
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1..11
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 CCCCTTCCTAA 22
|||||
Db 1 CCCCACCTAA 11

RESULT 206
AX711117
LOCUS AX711117 11 bp RNA linear PAT 11-APR-2003
DEFINITION Sequence 417 from Patent EP1288296.
ACCESSION AX711117
VERSION AX711117.1 GI:29787498
KEYWORDS
SOURCE Herpes simplex virus unknown type
ORGANISM Herpes simplex virus unknown type
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Simplexvirus.
1
REFERENCE
AUTHORS Draper,K.G., Mcswiggen,J.A., Holecck,J.J., Dudycz,L.W.,
Macejak,D.G. and Mamone,J.A.
TITLE Method and reagent for inhibiting HBV viral replication
JOURNAL Patent: EP 1288296-A 417 05-MAR-2003;

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FEATURES
source
1. .11
RIBOZYME PHARMACEUTICALS, INC. (US)
Location/Qualifiers

/organism="Herpes simplex virus unknown type"
/mol_type="unassigned RNA"
/db_xref="taxon:126283"

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
| | | | | | | |
Db 1 CCCCCCTGCCT 11

RESULT 207
BD001258
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BD001258 11 bp RNA linear PAT 31-JAN-2002
Method and reagent for inhibiting viral replication.

Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J., and Mamone, A.J.
Method and reagent for inhibiting viral replication
Patent: JP 2000342285-A 418 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342285-A/418
PD 12-DEC-2000
PP 01-MAY-2000 JP 2000132616

PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
14-MAY-1992 US 07/882889, 14-MAY-1992 US 07/882921 PR
14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/884073 PR
14-MAY-1992 US 07/883849, 14-MAY-1992 US 07/884333 PR
14-MAY-1992 US 07/884422, 14-MAY-1992 US 07/884431 PR
14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,

PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22, C12N15/10, C12R1:91, PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
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Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
| | | | | | | |
Db 1 CCCCCCTGCCT 11

RESULT 208

BD001687
LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BD001687 11 bp RNA linear PAT 31-JAN-2002
Method and reagent for inhibiting viral replication.

Draper, K.G., Dadyktz, L.W., Macswigen, J.A., Maysejak, D.G.,
Holesek, J.J., and Mamone, A.J.
Method and reagent for inhibiting viral replication
Patent: JP 2000342286-A 418 12-DEC-2000;
RIBOZYME PHARMACEUTICALS INC
OS Artificial Sequence
PN JP 2000342286-A/418
PD 12-DEC-2000
PP 01-MAY-2000 JP 2000132651

PR 11-MAY-1992 US 07/882689, 14-MAY-1992 US 07/882712 PR
14-MAY-1992 US 07/882713, 14-MAY-1992 US 07/882714 PR
14-MAY-1992 US 07/882823, 14-MAY-1992 US 07/882824 PR
14-MAY-1992 US 07/882886, 14-MAY-1992 US 07/882888 PR
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14-MAY-1992 US 07/882922, 14-MAY-1992 US 07/884073 PR
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14-MAY-1992 US 07/884436, 14-MAY-1992 US 07/884521 PR
31-JUL-1992 US 07/923738, 26-AUG-1992 US 07/935854 PR
26-AUG-1992 US 07/936086, 18-SEP-1992 US 07/948359 PR
15-OCT-1992 US 07/963322, 07-DEC-1992 US 07/987129 PR
07-DEC-1992 US 07/987130, 07-DEC-1992 US 07/987133 PI
KENNETH G DRAPER, LEC W DADYKTZ, JAMES A MACSWIGEN, PI DENNIS G
MAYSEJAK,

PI JAMES J HOLESEK, ANTHONY J MAMONE
PC C12N15/09, C12N5/10, C12N7/00, C12N9/22, C12N15/10, C12R1:91, PC
C12N15/00,
PC C12N5/00, (C12N5/00, C12R1:91)
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Best Local Similarity 81.8%; Pred. No. 96;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
| | | | | | | |
Db 1 CCCCCCTGCCT 11

RESULT 209

BD091501/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

BD091501
Transcriptional activator.

BD091501.1 GI:22637112
WO 0132860-A/2.
synthetic construct

ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 13)
AUTHORS Kataoka, K.
TITLE Transcriptional activator
JOURNAL Patent: WO 0132860-A 2 10-MAY-2001;
COMMENT OTSUKA PHARMACEUTICAL CO LTD, KOSUKE KATAOKA
OS Artificial Sequence
PN WO 0132860-A/2
PD 10-MAY-2001
PF 15-FEB-2000 WO 2000JP000841
PR 04-NOV-1999 JP 99P 314335
PI KOSUKE KATAOKA
PC C12N15/11,C01G11/00,C01G13/04,C01G7/00,C07C323/52,C07H23/00 CC
FH Key Location/Qualifiers.
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Best Local Similarity 81.8%; Pred. No. 1.1e+02;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 15 CTTCTTAAGCA 25
Db 11 CTTAGTAGCA 1
RESULT 210
AR124568/c
LOCUS AR124568 10 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 14 from patent US 6171864.
ACCESSION AR124568
VERSION AR124568.1 GI:14109929
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Coughlan, S.J. and Winfrey, R.J. Jr.
TITLE Calcitriol genes and promoter regions and uses thereof
JOURNAL Patent: US 6171864-A 14 09-JAN-2001;
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
Query Match 29.2%; Score 7.6; DB 1; Length 10;
Best Local Similarity 70.0%; Pred. No. 95;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 CCACCTCATC 10
Db 10 YCAYTCATC 1
RESULT 211
AR11385
LOCUS AR11385 10 bp DNA linear PAT 05-MAR-1997
DEFINITION Sequence 11 from Patent WO9426928.
ACCESSION AR11385
VERSION AR11385.1 GI:2297104
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Strauss, M. and Bauer, D.
TITLE COMPLEX DIAGNOSTIC AGENT OF GENETIC EXPRESSION AND MEDICAL
DIAGNOSIS AND GENE ISOLATION PROCESS USING SAID DIAGNOSTIC AGENT

JOURNAL Patent: WO 9426928-A 11 24-NOV-1994;
COMMENT MAX PLANCK GESELLSCHAFT (DE)
FEATURES Other publication DE 4317414 940421.
source Location/Qualifiers
1..10
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 TTCCTAAGC 24
Db 1 TACCTAAGC 9
RESULT 212
AS2289
LOCUS AS2289 10 bp DNA linear PAT 12-DEC-1997
DEFINITION Sequence 79 from Patent EP0705842.
ACCESSION AS2289
VERSION AS2289.1 GI:2852024
KEYWORDS
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1
AUTHORS Bartnik, E.D. and Margerie, D.D.
TITLE Regulated genes by stimulation of chondrocytes with 1L-1beta
JOURNAL Patent: EP 0705842-A 79 10-APR-1996;
COMMENT HOECHST AG (DE)
Other publication ZA 9508381 960424
Other publication JP 8191693 960730
Other publication CA 2159957 960407
Other publication AU 3308695 960418.
FEATURES Location/Qualifiers
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 16 TTCCTAAGC 24
Db 1 TACCTAAGC 9
RESULT 213
AR027855/c
LOCUS AR027855 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 53 from patent US 5856459.
ACCESSION AR027855
VERSION AR027855.1 GI:5938675
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Frank, B.L., Roberts, P.C., Goodchild, J., Craig, J. Charles. and
Mills, J.S.
TITLE Oligonucleotides specific for hepatitis B virus
JOURNAL Patent: US 5856459-A 53 05-JAN-1999;
FEATURES Location/Qualifiers
source
1..10
/organism="unknown"
/mol_type="unassigned DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;

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Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 9 TCGCCCCCTT 17
Db 10 TCGACCTT 2

RESULT 214
AR028295/c
LOCUS AR028295 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 5 from patent US 5858662.
ACCESSION AR028295
VERSION AR028295.1 GI:5940268
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Keating,M.T. and Morris,C.A.
TITLE Diagnosis of Williams syndrome and Williams syndrome cognitive
JOURNAL profile by analysis of the presence or absence of a LIM-kinase gene
FEATURES Patent: US 5858662-A 5 12-JAN-1999;
Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 1 CCACCTCAT 9
Db 9 CACCTCAT 1

RESULT 215
AR030091/c
LOCUS AR030091 10 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 280 from patent US 5861244.
ACCESSION AR030091
VERSION AR030091.1 GI:5943305
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Wang,C.-G. and Hepburn,A.G.
TITLE Genetic sequence assay using DNA triple strand formation
JOURNAL Patent: US 5861244-A 280 19-JAN-1999;
FEATURES Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 12 CCCCTTCTT 20
Db 1 CCCCTTCTT 9

RESULT 216
AR092702/c
LOCUS AR092702 10 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 14 from patent US 5998193.
ACCESSION AR092702
VERSION AR092702.1 GI:10019454
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
REFERENCE
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 5998193-A 14 07-DEC-1999;
Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 9 TCGCCCCCTT 17
Db 9 TCCCCCTT 1

RESULT 217
AR106686/c
LOCUS AR106686 10 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 14 from patent US 6107078.
ACCESSION AR106686
VERSION AR106686.1 GI:12821216
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
AUTHORS Keese,P., Stapper,M. and Perriman,R.
TITLE Ribozymes with optimized hybridizing arms, stems, and loops, tRNA
JOURNAL embedded ribozymes and compositions thereof
FEATURES Patent: US 6107078-A 14 22-AUG-2000;
Location/Qualifiers
source 1..10
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Indels 1; Gaps 0;
Matches 8; Conservative 0;

Qy 9 TCGCCCCCTT 17
Db 9 TCCCCCTT 1

RESULT 218
BD065077/c
LOCUS BD065077 10 bp DNA linear PAT 27-AUG-2002
DEFINITION Characterization of the yeast transcriptome.
ACCESSION BD065077
VERSION BD065077.1 GI:22610680
KEYWORDS Saccharomyces cerevisiae (baker's yeast)
SOURCE Saccharomyces cerevisiae
ORGANISM Eukaryota; Fungi; Ascomycota; Saccharomycetaceae; Saccharomycetes;
REFERENCE Velculescu,V.E., Vogelstein,B. and Kinzler,K.W.
AUTHORS Characterization of the yeast transcriptome
TITLE Patent: JP 2001509017-A 13 10-JUL-2001;
JOURNAL THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT OS Saccharomyces cerevisiae (yeast)
PN JP 2001509017-A/13
PD 10-JUL-2001
PF 22-JAN-1998 JP 1998532117
PR 23-JAN-1997 US 60/035917
PI VICTOR E VELCULESCU, BERT VOGELSTEIN, KENNETH W KINZLER PC
C12N15/10, C12N15/31, C07K14/395, C12Q1/68, C12Q1/02 CC

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Characterization of the yeast transcriptome
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Saccharomyces cerevisiae (yeast)'.
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1..10 Location/Qualifiers
/organism='Saccharomyces cerevisiae'
/mol_type='genomic DNA'
/db_xref='taxon:4932'
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 8 ATCGGCCCT 16
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DB 1 ATCGCGCT 9
RESULT 219
BD161370/C
LOCUS BD161370 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human activated Th1 and Th2 cell expression genes.
ACCESSION BD161370
VERSION BD161370.1 GI:27867128
KEYWORDS JP 2002186482-A/192.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Nagai,S., Matsushima,K. and Hashimoto,S.
TITLE Human activated Th1 and Th2 cell expression genes
JOURNAL Patent: JP 2002186482-A 192 02-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002186482-A/192
PD 02-JUL-2002
PF 19-DEC-2000 JP 2000385816
PI SHIGENORI NAGAI,KOJI MATSUSHIMA,SHINICHI HASHIMOTO PC
C12N15/09,C07K14/47,C07K16/18,C12P21/08,C12N15/00 CC Human
activated Th1 and Th2 cell expression genes FH Key
Location/Qualifiers 1..10
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1..10 Location/Qualifiers
/organism='Homo sapiens'
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/db_xref='taxon:9606'
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
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DB 10 CCCGTCCT 2
RESULT 220
BD166733/C
LOCUS BD166733 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166733
VERSION BD166733.1 GI:27872545
KEYWORDS JP 200209591-A/278.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.

Human liver disease-expressing genes
Patent: JP 200209591-A 278 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 200209591-A/278
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
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CC Human liver disease-expressing genes
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/mol_type='genomic DNA'
/db_xref='taxon:32644'
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
|||||
DB 10 CCCGTCCT 2
RESULT 221
BD166772/C
LOCUS BD166772 10 bp DNA linear PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166772
VERSION BD166772.1 GI:27872584
KEYWORDS JP 200209591-A/317.
SOURCE unidentified
ORGANISM unidentified
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 200209591-A 317 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 200209591-A/317
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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/db_xref='taxon:32644'
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 17 TCCTAAGCA 25
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DB 10 TCCAAAGCA 2

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RESULT 222
BD166789/c
LOCUS      BD166789          10 bp      DNA          linear          PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166789
VERSION    BD166789.1 GI:27872601
KEYWORDS   JP 2002209591-A/334.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 334 30-JUL-2002;
           JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
           PN JP 2002209591-A/334
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
           YAMASHITA
           PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
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           PC C12N15/00
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATCGCCCC 15
Db 10 CATCTCCCC 2

RESULT 223
BD166809
LOCUS      BD166809          10 bp      DNA          linear          PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166809
VERSION    BD166809.1 GI:27872621
KEYWORDS   JP 2002209591-A/354.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 354 30-JUL-2002;
           JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
           PN JP 2002209591-A/354
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
           YAMASHITA
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Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATCGCCCC 15
Db 10 CATCTCCCC 2

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Query Match      28.5%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 CTCATCGCC 13
Db 1 CCCATCGCC 9

RESULT 224
BD166820
LOCUS      BD166820          10 bp      DNA          linear          PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166820
VERSION    BD166820.1 GI:27872632
KEYWORDS   JP 2002209591-A/365.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 365 30-JUL-2002;
           JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)
           PN JP 2002209591-A/365
           PD 30-JUL-2002
           PF 19-JAN-2001 JP 2001012328
           PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
           YAMASHITA
           PC C12N15/09, C07K14/47, C07K16/18, G01N33/15, G01N33/50//C12P21/02,
           C12P21/08,
           PC C12N15/00
           CC Human liver disease-expressing genes
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           FT source 1..10
           FT /organism='Homo sapiens (human)'.

FEATURES
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           /db_xref="taxon:32644"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
Db 1 ACATCATCG 9

RESULT 225
BD166995/c
LOCUS      BD166995          10 bp      DNA          linear          PAT 17-JAN-2003
DEFINITION Human liver disease-expressing genes.
ACCESSION  BD166995
VERSION    BD166995.1 GI:27872807
KEYWORDS   JP 2002209591-A/540.
SOURCE     unidentified
ORGANISM   unclassified.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE      Human liver disease-expressing genes
JOURNAL    Patent: JP 2002209591-A 540 30-JUL-2002;
           JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT    OS Homo sapiens (human)

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PN JP 2002209591-A/540
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
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FT Location/Qualifiers
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TCCTAAGCA 25
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Db 10 TCCAAAGCA 2

RESULT 226
BD166996/c
LOCUS
DEFINITION Human liver disease-expressing genes.
ACCESSION BD166996
VERSION BD166996.1 GI:27872808
KEYWORDS JP 2002209591-A/541.
SOURCE unidentified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima,K., Hashimoto,S., Kaneko,S. and Yamashita,T.
TITLE Human liver disease-expressing genes
JOURNAL Patent: JP 2002209591-A 541 30-JUL-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT OS Homo sapiens (human)
PN JP 2002209591-A/541
PD 30-JUL-2002
PF 19-JAN-2001 JP 2001012328
PI KOJI MATSUSHIMA,SHINICHI HASHIMOTO,SHUICHI KANEKO,TARO PI
YAMASHITA
PC C12N15/09,C07K14/47,C07K16/18,G01N33/15,G01N33/50//C12P21/02,
C12P21/08,
PC C12N15/00
CC Human liver disease-expressing genes
FH Key Location/Qualifiers
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FT Location/Qualifiers
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 CATCGCCCC 15
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Db 10 CATCTCCCC 2

RESULT 227
BD225340/c
LOCUS
DEFINITION Compositions and methods for the identification of lung tumor
cells.
ACCESSION BD225340
VERSION BD225340.1 GI:33035110
KEYWORDS JP 2002509707-A/22.
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
1 (bases 1 to 10)
Beaudry,G.A., Madden,S.L. and Bertelsen,A.H.
Compositions and methods for the identification of lung tumor cells
Patent: JP 2002509707-A 22 02-APR-2002;
GENZYME CORP
OS Artificial Sequence
PN JP 2002509707-A/22
PD 02-APR-2002
PF 30-MAR-1999 JP 2000541180
PR 31-MAR-1998 US 60/080037
PI GARY A BEAUDRY,STEPHEN L MADDEN ARTHUR H BERTELSEN PC
C12N15/09,A01K67/027,C07H21/04,C07K14/47,C07K16/18,C12N1/15, PC
C12N1/19,
PC C12N1/21,C12N5/10,C12P21/08,C12Q1/68,G01N33/15,G01N33/53, PC
G01N33/566//
PC A61K45/00,A61P9/00,A61P35/00,C12N15/00,C12N5/00 CC
Compositions and methods for the identification of lung tumor CC
Cells
FH Key Location/Qualifiers
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    /organism='Artificial Sequence'.
FT Location/Qualifiers
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Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
    ||| |||||
Db 9 CTCCTCATC 1

RESULT 228
BD238638/c
LOCUS
DEFINITION Preparation and use of superior vaccines.
ACCESSION BD238638
VERSION BD238638.1 GI:33048408
KEYWORDS JP 2002534056-A/56.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 56 15-OCT-2002;
GENZYME CORP
OS Homo sapiens (human)
PN JP 2002534056-A/56
PD 15-OCT-2002
PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
19-JUN-1998 US 60/090035,19-JUN-1998 US 60/089993 PR
19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR

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Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Gaps 0; Indels 1; Length 10;

QY 14 CTTCTCTAA 22
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Db 2 CTTTCTAA 10

RESULT 231
BD239042/C
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 460 15-OCT-2002;
GENZYME CORP

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

OS Homo sapiens (human)
PN JP 2002534056-A/460
PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/089992,19-JUN-1998 US 60/090072 PR
19-JUN-1998 US 60/089878,19-JUN-1998 US 60/089991 PR
19-JUN-1998 US 60/090000,19-JUN-1998 US 60/090048 PR
19-JUN-1998 US 60/089999,19-JUN-1998 US 60/090043 PR
19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
19-JUN-1998 US 60/090080,19-JUN-1998 US 60/089833 PR
19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,

CC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FF Key Location/Qualifiers

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Query Match 28.5%; Score 7.4; DB 1; Length 10;

Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Gaps 0; Indels 1; Length 10;

Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Length 10;

QY 17 TCCTAGCA 25
|||||
Db 10 TCCTAGCA 2

RESULT 232
BD239478
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 460 15-OCT-2002;
GENZYME CORP

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 896 15-OCT-2002;
GENZYME CORP

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

OS Homo sapiens (human)
PN JP 2002534056-A/896
PD 15-OCT-2002

PF 18-JUN-1999 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR

PI BRUCE L ROBERTS,SRINIVAS SHANKARA
PC C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15, PC
C12N1/19,

PC C12N1/21,C12N5/10,G01N33/15,G01N33/50,G01N33/53,G01N33/566, PC
G01N37/00,

CC C12N15/00,C12N5/00,C12N15/00

CC Preparation and use of superior vaccines

FF Key Location/Qualifiers

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FT /organism='Homo sapiens (human)'. .

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1. .10

/organism='Homo sapiens'

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Best Local Similarity 88.9%; Pred. No. 1e+02; Mismatches 0; Gaps 0; Indels 1; Length 10;

Matches 8; Conservative 0; Mismatches 0; Gaps 0; Indels 1; Length 10;

QY 3 ACCTCATCG 11

|||||

Db 1 ACCCCATCG 9

RESULT 233

BD239549

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 10)
Roberts,B.L. and Shankara,S.
Preparation and use of superior vaccines
Patent: JP 2002534056-A 967 15-OCT-2002;
GENZYME CORP

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

G01N37/00,									
PC	C12N15/00,C12N5/00,C12N15/00								
CC	Preparation and use of superior vaccines								
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Db	10 CTCAACGCC 2								
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LOCUS	BD239667	10 bp	DNA	linear					PAT 17-JUL-2003
DEFINITION	Preparation and use of superior vaccines.								
ACCESSION	BD239667								
VERSION	BD239667.1 GI:33049437								
KEYWORDS	JP 2002534056-A/1085.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
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	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;								
	Hominidae; Homo								
REFERENCE	1 (bases 1 to 10)								
AUTHORS	Roberts,B.L. and Shankara,S.								
TITLE	Preparation and use of superior vaccines								
JOURNAL	Patent: JP 2002534056-A 1085 15-OCT-2002;								
	GENZYME CORP								
COMMENT	OS Homo sapiens (human)								
	PN JP 2002534056-A/1085								
	PD 15-OCT-2002								
	PF 18-JUN-1999 JP 2000554749								
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	19-JUN-1998 US 60/090076,19-JUN-1998 US 60/090045 PR								
	08-DEC-1998 US 60/111715								
	PI BRUCE L ROBERTS,SRINIVAS SHANKARA								
PC	C12N15/09,C12N15/09,A61K39/00,A61P35/00,A61P37/04,C12N1/15,PC								
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G01N37/00,									
PC	C12N15/00,C12N5/00,C12N15/00								
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Best Local Similarity	88.9%; Pred.No.1e+02; Indels 0; Gaps 0;								

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DEFINITION Preparation and use of superior vaccines.
ACCESSION BD240481
VERSION BD240481.1 GI:33050251
KEYWORDS JP 2002534056-A/1899.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
AUTHORS Roberts,B.L. and Shankara,S.
TITLE Preparation and use of superior vaccines
JOURNAL Patent: JP 2002534056-A 1899 15-OCT-2002;
GENZYME CORP
COMMENT
OS Homo sapiens (human)
PN JP 2002534056-A/1899
PD 15-OCT-2002
PF 18-JUN-1998 JP 2000554749
PR 19-JUN-1998 US 60/090039,19-JUN-1998 US 60/090040 PR
19-JUN-1998 US 60/090041,19-JUN-1998 US 60/089853 PR
19-JUN-1998 US 60/089997,19-JUN-1998 US 60/090079 PR
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19-JUN-1998 US 60/090042,19-JUN-1998 US 60/090036 PR
19-JUN-1998 US 60/090044,19-JUN-1998 US 60/089844 PR
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19-JUN-1998 US 60/089994,19-JUN-1998 US 60/090077 PR
19-JUN-1998 US 60/090078,19-JUN-1998 US 60/090047 PR
08-DEC-1998 US 60/090076,19-JUN-1998 US 60/090045 PR
PI BRUCE L ROBERTS, SRINIVAS SHANKARA
PC C12N15/09, C12N15/10, G01N33/15, G01N33/50, G01N33/53, G01N33/566, PC
C12N1/19, G01N37/00,
PC C12N15/00, C12N5/00, C12N15/00
CC Preparation and use of superior vaccines
FH Key Location/Qualifiers
FT source 1..10
FT /organism='Homo sapiens (human)'.
FEATURES
source
1..10
Location/Qualifiers
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/db_xref='taxon:9606'
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No.1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 CCTCATCGC 12
DB 9 CCCCATCGC 1
RESULT 240
LOCUS BD242837
DEFINITION Microassay for continuous analysis of gene expression and its
application.
ACCESSION BD242837
VERSION BD242837.1 GI:33052607
KEYWORDS JP 2002535012-A/27.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cheval,L., Elalouf,J.M. and Virlon,B.
TITLE Microassay for continuous analysis of gene expression and its
application
JOURNAL Patent: JP 2002535012-A 27 22-OCT-2002;
COMMISSARIAT A L'ENERGIE ATOMIQUE, CENTRE NATIONAL DE LA RECHERCHE
SCIENTIFIQUE
COMMENT
OS Artificial Sequence
PN JP 2002535012-A/27
PD 22-OCT-2002
PF 25-JAN-2000 JP 2000596176
PR 27-JAN-1999 EP 99400189.9
PI LYDIE CHEVAL, JEAN MARC ELALOUF, BERANGERE VIRLON PC
C12N15/09, C12Q1/68, C12N15/00
CC Description of Artificial Sequence:linker
FH Key Location/Qualifiers

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        Location/Qualifiers
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            /db_xref="taxon:32630"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
Db 1 GTCCCTTCC 9

RESULT 241
CQ483558/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Homo sapiens (human)
    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
    1
    Schlegel,R., Endege,W.O. and Monahan,J.E.
    Genes differentially expressed in human prostate cancer and their
    use
    Patent: WO 0160860-A 15425 23-AUG-2001;
    Millennium Predictive Medicine, Inc. (US)
FEATURES
    source
        Query Match 28.5%; Score 7.4; DB 1; Length 10;
        Best Local Similarity 88.9%; Pred. No. 1e+02;
        Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
Db 9 GCCCCTACC 1

RESULT 242
CQ857806
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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    Homo sapiens
    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
    Hominidae; Homo.
REFERENCE
    1
    Figtree,G.A., Farral,M., Channon,K. and Watkins,H.
    Diagnosis of an estrogen-sensitive disorder
    Patent: WO 2004070059-A 65 19-AUG-2004;
    ISIS INNOVATION LIMITED (GB)
FEATURES
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        Query Match 28.5%; Score 7.4; DB 1; Length 10;
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        Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
Db 9 GCCCCTACC 1

RESULT 243
CQ5050730/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
    Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
    Compositions, methods, and kits for fabricating coded molecular
    tags
    Patent: WO 2005021755-A 15 10-MAR-2005;
    Applera Corporation (US)
FEATURES
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        Query Match 28.5%; Score 7.4; DB 1; Length 10;
        Best Local Similarity 88.9%; Pred. No. 1e+02;
        Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCT 20
Db 9 CCCCTTCTCT 1

RESULT 244
CQ5050731
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
    Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C.,
    Ermakov,S., Hyldig-Nielsen,J., Schroeder,B., Vatta,P. and Bloch,W.
    Compositions, methods, and kits for fabricating coded molecular
    tags
    Patent: WO 2005021755-A 16 10-MAR-2005;
    Applera Corporation (US)
FEATURES
    source
        Query Match 28.5%; Score 7.4; DB 1; Length 10;
        Best Local Similarity 88.9%; Pred. No. 1e+02;
        Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCT 20
Db 9 CCCCTTCTCT 1

RESULT 245
CQ5050731
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
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    Compositions, methods, and kits for fabricating coded molecular
    tags
    Patent: WO 2005021755-A 16 10-MAR-2005;
    Applera Corporation (US)
FEATURES
    source
        Query Match 28.5%; Score 7.4; DB 1; Length 10;
        Best Local Similarity 88.9%; Pred. No. 1e+02;
        Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCTCT 20
Db 9 CCCCTTCTCT 1

```

```

Db          ||||| ||
            2 CCCCTTCT 10

RESULT 245
CS050762/c
LOCUS      CS050762      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION Sequence 15 from Patent WO2005021804.
ACCESSION  CS050762
VERSION     CS050762.1  GI:61889965
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C., Ermakov,S.
TITLE       Multiplex detection compositions, methods, and kits
JOURNAL     Patent: WO 2005021804-A 15 10-MAR-2005;
            Applera Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        ||||| ||
        9 CCCCTTCT 1

RESULT 246
CS050763
LOCUS      CS050763      10 bp      DNA      linear      PAT 23-MAR-2005
DEFINITION Sequence 16 from Patent WO2005021804.
ACCESSION  CS050763
VERSION     CS050763.1  GI:61889966
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C., Ermakov,S.
TITLE       Multiplex detection compositions, methods, and kits
JOURNAL     Patent: WO 2005021804-A 16 10-MAR-2005;
            Applera Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        ||||| ||
        9 CCCCTTCT 1

RESULT 247
CS056329/c
LOCUS      CS056329      10 bp      DNA      linear      PAT 04-APR-2005
DEFINITION Sequence 15 from Patent WO2005024021.
ACCESSION  CS056329
VERSION     CS056329.1  GI:62241969
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C. and
            Ermakov,S.
TITLE       Compositions, methods, and kits for assembling probes comprising
            coded molecular tags
JOURNAL     Patent: WO 2005024021-A 15 17-MAR-2005;
            Applera Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        ||||| ||
        2 CCCCTTCT 10

RESULT 249
E54779
LOCUS      E54779      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION  E54779
VERSION     E54779.1  GI:22556262
KEYWORDS    JP 2001211883-A/131.
SOURCE      Homo sapiens (human)

```

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DEFINITION Sequence 15 from Patent WO2005024021.
ACCESSION  CS056329
VERSION     CS056329.1  GI:62241969
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C. and
            Ermakov,S.
TITLE       Compositions, methods, and kits for assembling probes comprising
            coded molecular tags
JOURNAL     Patent: WO 2005024021-A 15 17-MAR-2005;
            Applera Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        ||||| ||
        9 CCCCTTCT 1

RESULT 248
CS056330
LOCUS      CS056330      10 bp      DNA      linear      PAT 04-APR-2005
DEFINITION Sequence 16 from Patent WO2005024021.
ACCESSION  CS056330
VERSION     CS056330.1  GI:62241970
KEYWORDS    .
SOURCE      synthetic construct
ORGANISM    other sequences; artificial sequences.
REFERENCE   1
AUTHORS     Woudenberg,T., Bahatt,D., Sharaf,M., Liu,T., Connell,C. and
            Ermakov,S.
TITLE       Compositions, methods, and kits for assembling probes comprising
            coded molecular tags
JOURNAL     Patent: WO 2005024021-A 16 17-MAR-2005;
            Applera Corporation (US)
FEATURES    Location/Qualifiers
            source
            1..10
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Description of Artificial Sequence: Synthetic oligonucleotide"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches          8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      12 CCCCTTCT 20
        ||||| ||
        2 CCCCTTCT 10

RESULT 249
E54779
LOCUS      E54779      10 bp      DNA      linear      PAT 27-AUG-2002
DEFINITION Human normal liver cell expression genes.
ACCESSION  E54779
VERSION     E54779.1  GI:22556262
KEYWORDS    JP 2001211883-A/131.
SOURCE      Homo sapiens (human)

```

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Homo.
REFERENCE 1 (bases 1 to 10)
AUTHORS Matsushima, K., Hashimoto, S., Kaneko, S. and Yamashita, T.
TITLE Human normal liver cell expression genes
JOURNAL Patent: JP 2001211883-A 131 07-AUG-2001;
SCIENCE & TECH AGENCY
COMMENT OS Homo sapiens (human)
PN JP 2001211883-A/131
PD 07-AUG-2001
PI 31-JAN-2000 JP 2000023170
PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, SHUICHI KANEKO, TARO PI
YAMASHITA
PC C12N15/09, C07K16/18, C12P21/02, C12N15/00
CC
FH Key Location/Qualifiers.
FEATURES
source 1..10
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 ACCTCATCG 11
||| |||||
Db 1 ACATCATCG 9
RESULT 250
AR234531
LOCUS AR234531 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 65 from patent US 6458584.
ACCESSION AR234531
VERSION AR234531.1 GI:272777235
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Mirzabekov, A., Guschin, D.Y., Chik, V., Drobyshch, A., Fotin, A.,
Yerzhanov, G. and Lysov, Y.
TITLE Customized oligonucleotide microchips that convert multiple genetic
information to simple patterns, are portable and reusable
JOURNAL Patent: US 6458584-A 65 01-OCT-2002;
University of Chicago; Chicago, IL
FEATURES
source 1..10
Location/Qualifiers
/organism="genomic DNA"
/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CACCTCATC 10
||| |||||
Db 1 CTCCTCATC 9
RESULT 251
AR236019
LOCUS AR236019 10 bp DNA linear PAT 20-DEC-2002
DEFINITION Sequence 16 from patent US 6461871.
ACCESSION AR236019
VERSION AR236019.1 GI:27279404
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
1 (bases 1 to 10)
Kubista, M., Svanvik, N. and Westman, G.
Method for the preparation of a probe for nucleic acid
hybridization
Patent: US 6461871-A 16 08-OCT-2002;
Lightup Technologies AB, Huddinge;
SEX;
FEATURES
source 1..10
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 12 CCCCTTCCT 20
||| |||||
Db 1 CCTCTTCCT 9
RESULT 252
AR266776
LOCUS AR266776 10 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 139 from patent US 6495336.
ACCESSION AR266776
VERSION AR266776.1 GI:29695849
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Ludin, C., Wikstroem, P., Svendsen, L.G. and Schulze, A.
TITLE Oligopeptide derivatives for the electrochemical measurement of
protease activity
JOURNAL Patent: US 6495336-A 139 17-DEC-2002;
Pentapharm AG;;
CHX;
FEATURES
source 1..10
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 18 CCTAAGCAT 26
||| |||||
Db 2 CCCAAGCAT 10
RESULT 253
AR274332
LOCUS AR274332 10 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 28 from patent US 6506561.
ACCESSION AR274332
VERSION AR274332.1 GI:29706778
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 10)
AUTHORS Cheval, L., Elalouf, J.-M. and Wirlon, B.
TITLE Method of obtaining a library of tags capable of defining a
specific state of a biological sample
JOURNAL Patent: US 6506561-A 28 14-JAN-2003;
Commissariat a l'Energie Atomique and Centre National de la
Recherche Scientifique-CNRS; Paris;
FRX;
FEATURES
source 1..10
Location/Qualifiers


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/organism="unknown"
/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
Db 1 GTCCCTTCC 9

RESULT 254
LOCUS AR303698 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 423 from patent US 6544736.
ACCESSION AR303698
VERSION AR303698.1 GI:31692474
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 423 08-APR-2003; Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGC 24
Db 1 TACCTAAGC 9

RESULT 255
LOCUS AR303732 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 457 from patent US 6544736.
ACCESSION AR303732
VERSION AR303732.1 GI:31692508
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 457 08-APR-2003; Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGC 24
Db 1 TACCTAAGC 9

RESULT 256
LOCUS AR303739/c 10 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 464 from patent US 6544736.
ACCESSION AR303739
VERSION AR303739.1 GI:31692515
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Shimamoto,A., Furuichi,Y., Shibata,Y., Funaki,H., Ohara,E. and Watahiki,M.
TITLE Method for synthesizing cDNA from mRNA sample
JOURNAL Patent: US 6544736-A 464 08-APR-2003; Nippon Gene Co., Ltd. and Agene Research Institute Co., Ltd.; Tokyo; JPX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGC 24
Db 9 TTCGTAAGC 1

RESULT 257
LOCUS AR351719 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1261 from patent US 6588746.
ACCESSION AR351719
VERSION AR351719.1 GI:33753515
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10)
AUTHORS Dobrindt,D. and Fischer,U.
TITLE Device for generating an offset of transported flexible sheet material
JOURNAL Patent: US 6588746-A 1261 08-JUL-2003; NexPress Solutions LLC; Rochester, NY; DEX;

FEATURES
source Location/Qualifiers
1..10
/organism="unknown"
/mol_type="genomic DNA"

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
Db 9 CACCTCTTC 1

RESULT 258
LOCUS AR351721/c 10 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1263 from patent US 6588746.
ACCESSION AR351721
VERSION AR351721.1 GI:33753517
KEYWORDS

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SOURCE      Unknown.
ORGANISM     Unknown.
REFERENCE    Unclassified.
AUTHORS      1 (bases 1 to 10)
TITLE        Dobrindt,D. and Fischer,U.
JOURNAL      Device for generating an offset of transported flexible sheet
              material
              Patent: US 6588746-A 1263 08-JUL-2003;
              NexPress Solutions LLC; Rochester, NY;
              DEX;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          2 CACCTCATC 10
Db          9 CACCTCCTC 1
RESULT 259
AR351722/c
LOCUS       AR351722
DEFINITION Sequence 1264 from patent US 6588746.
ACCESSION  AR351722
VERSION     AR351722.1 GI:33753518
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Dobrindt,D. and Fischer,U.
TITLE      Device for generating an offset of transported flexible sheet
              material
              Patent: US 6588746-A 1264 08-JUL-2003;
              NexPress Solutions LLC; Rochester, NY;
              DEX;
FEATURES     Location/Qualifiers
              1..10
              /organism="unknown"
              /mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          2 CACCTCATC 10
Db          9 CACCTCCTC 1
RESULT 260
AR364130
LOCUS       AR364130
DEFINITION Sequence 10 from patent US 5256545.
ACCESSION  AR364130
VERSION     AR364130.1 GI:34426456
KEYWORDS   .
SOURCE     Unknown.
ORGANISM   Unknown.
REFERENCE  1 (bases 1 to 10)
AUTHORS    Brown,M.S., Goldstein,J.L., Russell,D.W. and Sudhof,T.C.
TITLE      Sterol Regulatory Elements
              Patent: US 5256545-A 10 26-OCT-1993;
              Board of Regents, The University of Texas System; Austin, TX
              Location/Qualifiers
              1..10
              /organism="unknown"

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/mol_type="genomic DNA"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          18 CCTAAGCAT 26
Db          1 CCTATGCAT 9
RESULT 261
AX033052
LOCUS       AX033052
DEFINITION Sequence 27 from Patent EP1024201.
ACCESSION  AX033052
VERSION     AX033052.1 GI:10279955
KEYWORDS   .
SOURCE     synthetic construct
              other sequences; artificial sequences.
              ORGANISM
              1
              REFERENCE
              AUTHORS
              TITLE
              JOURNAL
              Patent: EP 1024201-A 27 02-AUG-2000;
              COMMISSARIAT ENERGIE ATOMIQUE (FR) ; DE CENTRE NAT (FR)
              Location/Qualifiers
              1..10
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="linker"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          11 GCCCCTTCC 19
Db          1 GTCCCTTCC 9
RESULT 262
AX152405/c
LOCUS       AX152405
DEFINITION Sequence 320 from Patent WO0138577.
ACCESSION  AX152405
VERSION     AX152405.1 GI:14534056
KEYWORDS   .
SOURCE     Homo sapiens (human)
              Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
              Hominidae; Homo.
              1
              REFERENCE
              AUTHORS
              TITLE
              JOURNAL
              Patent: WO 0138577-A 320 31-MAY-2001;
              The Johns Hopkins University (US)
              Location/Qualifiers
              1..10
              /organism="Homo sapiens"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9606"
Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY          12 CCCCTTCCT 20
Db          10 CCGTTCCT 2

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RESULT 263
AX152423
LOCUS AX152423 Sequence 338 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION
ACCESSION AX152423
VERSION AX152423.1 GI:14534074
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcripts
TITLE Patent: WO 0138577-A 338 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CAGCTCATC 10
DB 1 CAGCTCATC 9

RESULT 264
AX15257
LOCUS AX15257 Sequence 472 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION
ACCESSION AX15257
VERSION AX15257.1 GI:14534208
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcripts
TITLE Patent: WO 0138577-A 472 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCG 11
DB 1 ACATCATCG 9

RESULT 265
AX152574
LOCUS AX152574 Sequence 489 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION
ACCESSION AX152574
VERSION AX152574.1 GI:14534225
KEYWORDS

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SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcripts
TITLE Patent: WO 0138577-A 489 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
DB 2 GCCCCTTCC 10

RESULT 266
AX152575
LOCUS AX152575 Sequence 490 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION
ACCESSION AX152575
VERSION AX152575.1 GI:14534226
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcripts
TITLE Patent: WO 0138577-A 490 31-MAY-2001;
JOURNAL The Johns Hopkins University (US)
FEATURES
source
1. .10
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 1e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
DB 2 GCCCCTTCC 10

RESULT 267
AX152614/C
LOCUS AX152614 Sequence 529 from Patent WO0138577. 10 bp DNA linear PAT 22-JUN-2001
DEFINITION
ACCESSION AX152614
VERSION AX152614.1 GI:14534265
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
REFERENCE
1 Velculescu, V.E., Vogelstein, B. and Kinzler, K.W.
AUTHORS Human transcripts
TITLE Patent: WO 0138577-A 529 31-MAY-2001;
JOURNAL

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[illegible]

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LOCUS      AX301337      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 51 from Patent WO0185941.
ACCESSION  AX301337
VERSION     AX301337.1  GI:17382420
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 51 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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Db      1  ACATCATCG 9

RESULT 273
AX301502
LOCUS      AX301502      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 216 from Patent WO0185941.
ACCESSION  AX301502
VERSION     AX301502.1  GI:17382595
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 216 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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QY      3  ACCTCATCG 11
        || |||||
Db      1  ACATCATCG 9

RESULT 274
AX301503
LOCUS      AX301503      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 217 from Patent WO0185941.
ACCESSION  AX301503
VERSION     AX301503.1  GI:17382586
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE       Tumor markers in ovarian cancer
JOURNAL     Patent: WO 0175177-A 125 11-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES    Location/Qualifiers
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REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 217 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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RESULT 275
AX301539
LOCUS      AX301539      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 253 from Patent WO0185941.
ACCESSION  AX301539
VERSION     AX301539.1  GI:17382622
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Versteeg,R. and Caron,H.N.
TITLE       Myc targets
JOURNAL     Patent: WO 0185941-A 253 15-NOV-2001;
            Academisch Ziekenhuis bij de Universiteit van Amsterdam (NL)
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QY      2  CACCTCATC 10
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Db      2  CACCTCAGC 10

RESULT 276
AX302607/c
LOCUS      AX302607      10 bp      DNA      linear      PAT 30-NOV-2001
DEFINITION Sequence 125 from Patent WO0175177.
ACCESSION  AX302607
VERSION     AX302607.1  GI:17383134
KEYWORDS    Homo sapiens (human)
SOURCE      Homo sapiens
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominiidae; Homo.
REFERENCE   1
AUTHORS     Morin,P.J., Sherman-Baust,C.A., Pizer,E.S. and Hough,C.D.
TITLE       Tumor markers in ovarian cancer
JOURNAL     Patent: WO 0175177-A 125 11-OCT-2001;
            THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
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QY 2 CACCTCATC 10
DB 9 CTCCTCATC 1

RESULT 277
AX377234/c
LOCUS AX377234 10 bp DNA linear PAT 18-MAR-2002
DEFINITION Sequence 35 from Patent WO0212497.
ACCESSION AX377234
VERSION AX377234.1 GI:19573523
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Choi,J.Y., Kazemi,A. and Koshy,B.
TITLE Haplotypes of the nfkb1b gene
JOURNAL Patent: WO 0212497-A 35 14-FEB-2002;
GENAissance Pharmaceuticals, Inc. (US)
FEATURES source
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QY 6 TCATCGCCC 14
DB 10 TCCTCGCCC 2

RESULT 278
AX465374/c
LOCUS AX465374 10 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 42 from Patent WO0211761.
ACCESSION AX465374
VERSION AX465374.1 GI:21899737
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 42 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES source
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DB 11 |||||

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QY 2 CACCTCATC 10
DB 9 CACCTCATC 1

RESULT 279
AX667812/c
LOCUS AX667812 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1261 from Patent WO0242459.
ACCESSION AX667812
VERSION AX667812.1 GI:29291349
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1261 30-MAY-2002;
Sangamo Biosciences Inc. (US)
FEATURES source
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Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
DB 9 CACCTCCTC 1

RESULT 280
AX667814/c
LOCUS AX667814 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1263 from Patent WO0242459.
ACCESSION AX667814
VERSION AX667814.1 GI:29291351
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Liu,Q.
TITLE Position dependent recognition of gnn nucleotide triplets by zinc
fingers
JOURNAL Patent: WO 0242459-A 1263 30-MAY-2002;
Sangamo Biosciences Inc. (US)
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QY 2 CACCTCATC 10
DB 9 CACCTCCTC 1

RESULT 281
AX667815/c
LOCUS AX667815 10 bp DNA linear PAT 26-MAR-2003
DEFINITION Sequence 1264 from Patent WO0242459.
ACCESSION AX667815
VERSION AX667815.1 GI:29291352

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KEYWORDS      synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Liu, Q.
TITLE          Position dependent recognition of gnn nucleotide triplets by zinc
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JOURNAL        Patent: WO 0242459-A 1264 30-MAY-2002;
               Sangamo Biosciences Inc. (US)
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AX753477/c
LOCUS          AX753477              10 bp      DNA      linear      PAT 23-JUN-2003
DEFINITION     Sequence 22 from Patent EP1310556.
ACCESSION      AX753477
VERSION        AX753477.1 GI:32166237
KEYWORDS       synthetic construct
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Beaudry, G.A., Madden, S.L. and Bertelsen, A.H.
TITLE          Composition and methods for the identification of lung tumor cells
JOURNAL        Patent: EP 1310556-A 22 14-MAY-2003;
               GENZYME CORPORATION (US)
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Db            9 CTCCTCATC 1
RESULT 283
BD007796
LOCUS          BD007796              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION     LPS activated human monocyte expressing genes.
ACCESSION      BD007796
VERSION        BD007796.1 GI:18636169
KEYWORDS       Homo sapiens
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE          LPS activated human monocyte expressing genes
JOURNAL        Patent: JP 2001069993-A 72 21-MAR-2001;
               JAPAN SCIENCE AND TECHNOLOGY CORP
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Db            9 CTCCTCATC 1
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BD007796
LOCUS          BD007796              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION     LPS activated human monocyte expressing genes.
ACCESSION      BD007796
VERSION        BD007796.1 GI:18636169
KEYWORDS       Homo sapiens
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE          LPS activated human monocyte expressing genes
JOURNAL        Patent: JP 2001069993-A 72 21-MAR-2001;
               JAPAN SCIENCE AND TECHNOLOGY CORP

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COMMENT        OS Homo sapiens (human)
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               PD 21-MAR-2001
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               PI KOJI MATSUSHIMA, SHINICHI HASHIMOTO, TAKUJI SUZUKI PC
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RESULT 284
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LOCUS          BD007887              10 bp      DNA      linear      PAT 31-JAN-2002
DEFINITION     LPS activated human monocyte expressing genes.
ACCESSION      BD007887
VERSION        BD007887.1 GI:18636260
KEYWORDS       Homo sapiens
SOURCE         Homo sapiens
ORGANISM       Homo sapiens
REFERENCE      1 (bases 1 to 10)
AUTHORS        Matsushima, K., Hashimoto, S. and Suzuki, T.
TITLE          LPS activated human monocyte expressing genes
JOURNAL        Patent: JP 2001069993-A 163 21-MAR-2001;
               JAPAN SCIENCE AND TECHNOLOGY CORP
COMMENT        OS Homo sapiens (human)
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GenCore version 5.1.8
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OM nucleic - nucleic search, using sw model

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Searched: 126 seqs, 1353 residues

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Maximum Match 100%

Listing first 127 summaries

Database : issdb4*

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and is derived by analysis of the total score distribution.

SUMMARIES

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2	12.2	46.9	17	1	US-09-866-108A-242
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6	10.8	41.5	15	1	US-08-291-932A-153
7	10.8	41.5	15	1	US-08-291-932A-158
8	10.8	41.5	15	1	US-08-291-932A-162
9	10.8	41.5	15	1	US-08-363-240A-119
10	10.8	41.5	15	1	US-08-363-240A-120
11	9.8	37.7	13	1	US-09-724-857-35
12	9.4	36.2	12	1	US-09-196-523-49
13	9.4	36.2	13	1	US-10-129-192A-2
14	9	34.6	10	1	US-08-467-126-2
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17	8.8	33.8	12	1	US-08-623-891-31
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Sequence 134, Appl	1	US-09-874-601-134	12	32.3	8.4	35	Sequence 134, Appl
Sequence 3, Appl	1	PCT-US94-08023-3	12	32.3	8.4	36	Sequence 3, Appl
Sequence 16, Appl	1	US-08-796-899-16	10	30.8	8	37	Sequence 16, Appl
Sequence 20, Appl	1	US-08-796-899-20	10	30.8	8	38	Sequence 20, Appl
Sequence 21, Appl	1	US-08-796-899-21	10	30.8	8	39	Sequence 21, Appl
Sequence 20, Appl	1	US-09-534-366A-20	10	30.8	8	40	Sequence 20, Appl
Sequence 69, Appl	1	US-09-442-054A-69	10	30.8	8	41	Sequence 69, Appl
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Sequence 9, Appl	1	US-08-196-103A-9	11	30.8	8	43	Sequence 9, Appl
Sequence 9, Appl	1	US-08-357-396-9	11	30.8	8	44	Sequence 9, Appl
Sequence 9, Appl	1	US-08-386-141-9	11	30.8	8	45	Sequence 9, Appl
Sequence 14, Appl	1	US-08-227-180B-14	11	30.8	8	46	Sequence 14, Appl
Sequence 104, Appl	1	US-08-623-891-104	11	30.0	7.8	47	Sequence 104, Appl
Sequence 355, Appl	1	US-08-173-489C-355	11	30.0	7.8	48	Sequence 355, Appl
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Sequence 104, Appl	1	US-09-634-262-104	11	30.0	7.8	50	Sequence 104, Appl
Sequence 240, Appl	1	US-09-249-155A-240	11	30.0	7.8	51	Sequence 240, Appl
Patent No. 5494663	1	5494663-21	11	30.0	7.8	52	Patent No. 5494663
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Sequence 53, Appl	1	US-08-468-352-53	10	28.5	7.4	55	Sequence 53, Appl
Sequence 5, Appl	1	US-08-678-039A-5	10	28.5	7.4	56	Sequence 5, Appl
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Sequence 82, Appl	1	US-08-388-353-82	10	28.5	7.4	58	Sequence 82, Appl
Sequence 84, Appl	1	US-08-388-353-84	10	28.5	7.4	59	Sequence 84, Appl
Sequence 188, Appl	1	US-08-388-353-188	10	28.5	7.4	60	Sequence 188, Appl
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Sequence 190, Appl	1	US-08-388-353-190	10	28.5	7.4	62	Sequence 190, Appl
Sequence 192, Appl	1	US-08-388-353-192	10	28.5	7.4	63	Sequence 192, Appl
Sequence 280, Appl	1	US-08-388-353-280	10	28.5	7.4	64	Sequence 280, Appl
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Sequence 84, Appl	1	US-08-488-551B-84	10	28.5	7.4	67	Sequence 84, Appl
Sequence 188, Appl	1	US-08-488-551B-188	10	28.5	7.4	68	Sequence 188, Appl
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Sequence 192, Appl	1	US-08-488-551B-192	10	28.5	7.4	71	Sequence 192, Appl
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Sequence 14, Appl	1	US-08-765-257A-14	10	28.5	7.4	73	Sequence 14, Appl
Sequence 65, Appl	1	US-09-261-115-65	10	28.5	7.4	74	Sequence 65, Appl
Sequence 16, Appl	1	US-09-486-853-16	10	28.5	7.4	75	Sequence 16, Appl
Sequence 139, Appl	1	US-09-914-259-139	10	28.5	7.4	76	Sequence 139, Appl
Sequence 28, Appl	1	US-09-501-721A-28	10	28.5	7.4	77	Sequence 28, Appl
Sequence 423, Appl	1	US-09-508-753B-423	10	28.5	7.4	78	Sequence 423, Appl
Sequence 457, Appl	1	US-09-508-753B-457	10	28.5	7.4	79	Sequence 457, Appl
Sequence 464, Appl	1	US-09-508-753B-464	10	28.5	7.4	80	Sequence 464, Appl
Sequence 10, Appl	1	US-09-721-777-10	10	28.5	7.4	81	Sequence 10, Appl
Patent No. 5256545	1	5256545-10	10	28.5	7.4	82	Patent No. 5256545
Sequence 12, Appl	1	US-08-250-310-12	10	26.9	7	83	Sequence 12, Appl
Sequence 12, Appl	1	US-08-439-404-12	10	26.9	7	84	Sequence 12, Appl
Sequence 3, Appl	1	US-08-507-598-3	10	26.9	7	85	Sequence 3, Appl
Sequence 303, Appl	1	US-08-173-489C-303	10	26.9	7	86	Sequence 303, Appl
Sequence 12, Appl	1	US-08-545-253A-12	10	26.9	7	87	Sequence 12, Appl
Sequence 3, Appl	1	US-08-507-750-3	10	26.9	7	88	Sequence 3, Appl
Sequence 1, Appl	1	US-08-908-367-1	10	26.9	7	89	Sequence 1, Appl
Sequence 193, Appl	1	US-08-388-353-193	10	26.9	7	90	Sequence 193, Appl
Sequence 194, Appl	1	US-08-388-353-194	10	26.9	7	91	Sequence 194, Appl
Sequence 210, Appl	1	US-08-388-353-210	10	26.9	7	92	Sequence 210, Appl
Sequence 211, Appl	1	US-08-388-353-211	10	26.9	7	93	Sequence 211, Appl
Sequence 212, Appl	1	US-08-388-353-212	10	26.9	7	94	Sequence 212, Appl
Sequence 213, Appl	1	US-08-388-353-213	10	26.9	7	95	Sequence 213, Appl
Sequence 289, Appl	1	US-08-388-353-289	10	26.9	7	96	Sequence 289, Appl
Sequence 290, Appl	1	US-08-388-353-290	10	26.9	7	97	Sequence 290, Appl
Sequence 291, Appl	1	US-08-388-353-291	10	26.9	7	98	Sequence 291, Appl
Sequence 292, Appl	1	US-08-388-353-292	10	26.9	7	99	Sequence 292, Appl
Sequence 193, Appl	1	US-08-488-551B-193	10	26.9	7	100	Sequence 193, Appl
Sequence 210, Appl	1	US-08-488-551B-210	10	26.9	7	101	Sequence 210, Appl
Sequence 211, Appl	1	US-08-488-551B-211	10	26.9	7	102	Sequence 211, Appl
Sequence 212, Appl	1	US-08-488-551B-212	10	26.9	7	103	Sequence 212, Appl

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107      7 26.9 10 1 US-08-488-551B-213 Sequence 213, App
c 108      7 26.9 10 1 US-08-488-551B-289 Sequence 289, App
c 109      7 26.9 10 1 US-08-488-551B-290 Sequence 290, App
c 110      7 26.9 10 1 US-08-488-551B-291 Sequence 291, App
c 111      7 26.9 10 1 US-08-488-551B-292 Sequence 292, App
c 112      7 26.9 10 1 US-08-839-327-12 Sequence 12, Appl
c 113      7 26.9 10 1 US-08-719-337-12 Sequence 12, Appl
c 114      7 26.9 10 1 US-09-340-781B-12 Sequence 12, Appl
c 115      7 26.9 10 1 US-08-764-522A-3 Sequence 3, Appl
c 116      7 26.9 10 1 US-08-764-528-3 Sequence 3, Appl
c 117      7 26.9 10 1 US-08-872-859-3 Sequence 3, Appl
c 118      7 26.9 10 1 US-08-522-384-24 Sequence 24, Appl
c 119      7 26.9 10 1 US-09-030-156-27 Sequence 27, Appl
c 120      7 26.9 10 1 US-09-645-757-27 Sequence 27, Appl
c 121      7 26.9 10 1 US-09-229-007A-81 Sequence 81, Appl
c 122      7 26.9 10 1 US-09-508-753B-52 Sequence 52, Appl
c 123      7 26.9 10 1 US-09-508-753B-128 Sequence 128, App
c 124      7 26.9 10 1 US-10-108-280-27 Sequence 27, Appl
c 125      7 26.9 10 1 US-10-113-424-81 Sequence 81, Appl
c 126      7 26.9 10 1 US-09-875-453B-32 Sequence 32, Appl
c 127      7 26.9 10 1 US-08-956-518A-110 Sequence 110, App

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ALIGNMENTS

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RESULT 1
US-08-983-605-11
; Sequence 11, Application US/08983605A
; Patent No. 6720137
; GENERAL INFORMATION:
; APPLICANT: Roder, Marion
; TITLE OF INVENTION: Microsatellite Markers for Plants of the Species
; TITLE OF INVENTION: Triticum Aestivum and Tribe Triticaceae and the Use of
; TITLE OF INVENTION: Said Markers
; FILE REFERENCE: 2936.10400
; CURRENT APPLICATION NUMBER: US/08/983,605A
; CURRENT FILING DATE: 1998-05-01
; EARLIER APPLICATION NUMBER: DE 195 25 284.5
; EARLIER FILING DATE: 1995-06-28
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-08-983-605-11

```

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Query Match 49.2%; Score 12.8; DB 1; Length 18;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 CCACCTCATCGCCCT 16
Db 2 CGACCTGATCGCCCT 17

```

```

RESULT 2
US-09-866-108A-242
; Sequence 242, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25

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; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6686188
; SEQ ID NO 242
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-866-108A-242

Query Match 46.9%; Score 12.2; DB 1; Length 17;
Best Local Similarity 82.4%; Pred. No. 13;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCTCCT 20
Db 1 CATCCTCGCCCTCCT 17

RESULT 3
US-09-866-108A-7555/c
; Sequence 7555, Application US/09866108A
; Patent No. 6686188
; GENERAL INFORMATION:
; APPLICANT: GU, Yizhong
; APPLICANT: JI, Yonggang
; APPLICANT: PENN, Sharron G.
; APPLICANT: HANZEL, David K.
; APPLICANT: RANK, David R.
; APPLICANT: CHEN, Wensheng
; APPLICANT: SHANNON, Mark
; TITLE OF INVENTION: MYOSIN-LIKE GENE EXPRESSED IN HUMAN HEART AND MUSCLE
; FILE REFERENCE: AEOMICA-7
; CURRENT APPLICATION NUMBER: US/09/866,108A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30

```


RESULT 6

US-08-291-932A-153
; Sequence 153, Application US/08291932A
; Patent No. 5658780

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth G.
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS
TITLE OF INVENTION: RIBOZYME TREATMENT OF
DISEASES OR CONDITIONS

NUMBER OF SEQUENCES: 830

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/291,932A

FILING DATE: August 15, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/157

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 153:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-291-932A-153

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCTCTAAGC 24

Db 1 GUCCCUUCCUACG 14

RESULT 7

US-08-291-932A-158
; Sequence 158, Application US/08291932A
; Patent No. 5658780

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth G.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

NUMBER OF SEQUENCES: 830

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

COUNTRY: California

ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

MEDIUM TYPE: storage

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/291,932A

FILING DATE: August 15, 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA: including application

PRIOR APPLICATION DATA: described below:

APPLICATION NUMBER: 08/245,466

FILING DATE: May 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Warburg, Richard J.

REGISTRATION NUMBER: 32,327

REFERENCE/DOCKET NUMBER: 208/157

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 158:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-291-932A-158

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 64.3%; Pred. No. 20;
Matches 9; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 GCCCTTCTCTAAGC 24

Db 2 GUCCCUUCCUACG 15

RESULT 8

US-08-291-932A-162
; Sequence 162, Application US/08291932A
; Patent No. 5658780

GENERAL INFORMATION:

APPLICANT: Stinchcomb, Dan T.

APPLICANT: Draper, Kenneth G.

APPLICANT: McSwiggen, James

TITLE OF INVENTION: RIBOZYME TREATMENT OF

TITLE OF INVENTION: DISEASES OR CONDITIONS

TITLE OF INVENTION: RELATED TO LEVELS OF

TITLE OF INVENTION: NF-KB

NUMBER OF SEQUENCES: 830

CORRESPONDENCE ADDRESS:

ADDRESSEE: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Suite 4700

STATE: Los Angeles

CITY: California

```

; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291.932A
; FILING DATE: August 15, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER: 08/245,466
; FILING DATE: May 18, 1994
; APPLICATION NUMBER: 07/987,132
; FILING DATE: December 7, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 208/157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 162:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-291-932A-162

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Two

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Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 57.1%; Pred. No. 20;
Matches 8; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 7 CATCGCCCTTCT 20
||:|||||:
Db 2 CAUGGUCCUCCU 15

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```

RESULT 9
US-08-363-240A-119
; Sequence 119, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 119:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-363-240A-119

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGCCC 14
|||||:|||||
Db 2 CCACCUUCUGCCC 15

RESULT 10
US-08-363-240A-120
; Sequence 120, Application US/08363240A
; Patent No. 5705388
; GENERAL INFORMATION:
; APPLICANT: Couture, Larry
; APPLICANT: McSwiggen, James
; APPLICANT: Bisgaier, Charles
; APPLICANT: Pape, Michael
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: PREVENTION, INHIBITION OF
; TITLE OF INVENTION: PROGRESSION AND REGRESSION
; TITLE OF INVENTION: OF VASCULAR DISEASES
; NUMBER OF SEQUENCES: 1243
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/363,240A
; FILING DATE: December 23, 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 210/096
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 120:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-363-240A-120

Query Match 41.5%; Score 10.8; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCACCTCATCGGCC 14
|||: ||||
Db 1 CCACCUUCUGGCC 14

RESULT 11
US-09-724-857-35/c
; Sequence 35, Application US/09724857
; Patent No. 6855866
; GENERAL INFORMATION:
; APPLICANT: Weterings, Koen
; APPLICANT: Apuya, Nestor R.
; APPLICANT: Tatarinova, Tatiana
; APPLICANT: Goldberg, Robert B.
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Polynucleotides Useful for Modulating Transcription
; FILE REFERENCE: 023070-114700US
; CURRENT APPLICATION NUMBER: US/09/724,857
; CURRENT FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 35
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:H-AP56 forward
US-09-724-857-35

Query Match 37.7%; Score 9.8; DB 1; Length 13;
Best Local Similarity 84.6%; Pred. No. 24;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CCTTCCTAAGCAT 26
||||| |||||
Db 13 CCTTCATAAGCTT 1

RESULT 12
US-09-196-523-49/c
; Sequence 49, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-49

Query Match 36.2%; Score 9.4; DB 1; Length 12;
Best Local Similarity 90.9%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ACCTCATCGCC 13
||| |||||
Db 12 ACCGCATCGCC 2

RESULT 13
US-10-129-192A-2
; Sequence 2, Application US/10129192A
; Patent No. 6908761
; GENERAL INFORMATION:
; APPLICANT: KATAOKA, Kohsuke
; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR
; FILE REFERENCE: Q69817
; CURRENT APPLICATION NUMBER: US/10/129,192A
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: PCT/JP00/00841
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: JP 1999-314335
; PRIOR FILING DATE: 1999-11-04
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Maf recognition element
US-10-129-192A-2

Query Match 36.2%; Score 9.4; DB 1; Length 13;
Best Local Similarity 90.9%; Pred. No. 28;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 15 CTTCTTAAGCA 25
||| |||||
Db 3 CTTACTAAGCA 13

RESULT 14
US-08-467-126-2/c
; Sequence 2, Application US/08467126
; Patent No. 5776744
; GENERAL INFORMATION:
; APPLICANT: GLAZER, PETER M.
; APPLICANT: GEORGE, JAY
; APPLICANT: LIN, L. MICHAEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TITLE OF INVENTION: EFFECTING HOMOLOGOUS RECOMBINATION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORPHARM, INC.
; STREET: 200 PERRY PARKWAY
; CITY: GAITHERSBURG
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE-3.50 INCH, 1.44 Mb
; MEDIUM TYPE: STORAGE
; COMPUTER: APPLE MACINTOSH POWERBOOK 520
; OPERATING SYSTEM: MACINTOSH
; SOFTWARE: WORD PERFECT 3.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,126
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
US-08-467-126-2/c

;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KARTA, GLENN E.
;; REGISTRATION NUMBER: 30,649
;; REFERENCE/DOCKET NUMBER: PA-0030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-527-2058
;; TELEFAX: 301-208-6997
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-467-126-2

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
|||||
Db 9 CCCCTTCCT 1

RESULT 15
US-08-476-712-1/c
; Sequence 1, Application US/08476712
; Patent No. 5962426
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,712
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-476-712-1

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20

Db 9 CCCCTTCCT 1
|||||

RESULT 16
US-09-411-291-1/c
; Sequence 1, Application US/09411291
; Patent No. 6303376
; GENERAL INFORMATION:
; APPLICANT: Glazer, Peter, M.
; TITLE OF INVENTION: Triple-Helix Forming Oligonucleotides for
; Targeted Mutagenesis
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/411,291
; FILING DATE: 04-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/476,712
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU114
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-873-8794
; TELEFAX: (404)-873-8795
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-411-291-1

Query Match 34.6%; Score 9; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
|||||
Db 9 CCCCTTCCT 1

RESULT 17
US-08-623-891-31
; Sequence 31, Application US/08623891
; Patent No. 5795778
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles

STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,200
FILING DATE:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 12
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-623-891-31

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
|||:|||||
Db 1 CCUCCAGCCCC 12

RESULT 18
US-08-173-489C-262
Sequence 262, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 262:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from Frankia sp
DESCRIPTION: 23s region in Seq ID No. 5861244261
HYPOTHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 262 :FROM 1 TO 12
US-08-173-489C-262

Query Match 33.8%; Score 8.8; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 CCTCATCGCCCC 15
|||||:|||||
Db 1 CCTCTTCCCCC 12

RESULT 19
US-09-340-861-31
Sequence 31, Application US/09340861
Patent No. 6432704
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440


```
;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/233,608
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Spruill, W. Murray
; REGISTRATION NUMBER: 32,943
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8615
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-233-608-44
```

```
Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10
```

```
RESULT 23
US-08-887-480-44
; Sequence 44, Application US/08887480
; Patent No. 5814453
; GENERAL INFORMATION:
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5814453artis Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,480
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/722,187
; FILING DATE: 15-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1739/PCT/CIP
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
;
US-08-887-480-44

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATCGCCCC 15
Db 1 TTATCGCCCC 10

RESULT 24
US-08-173-489C-223/c
; Sequence 223, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 223:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 23s rRNA gene from Escherichia coli
; DESCRIPTION: (Accession # M25458) nucleotides 1410 to 1419
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Escherichia coli
; STRAIN: MR8600
; PUBLICATION INFORMATION:
; AUTHORS: Brantlant, C, Krol, A, Machatt, M, A,
; AUTHORS: Pouyet, J, Ebel, J P, Edwards, K, Koessel,
; AUTHORS: H.
; TITLE: Primary and secondary
```

```

; TITLE: structures of Escherichia coli MRE 600 23S
; TITLE: ribosomal RNA Comparison with models of
; TITLE: secondary structure for maize chloroplast 23S
; TITLE: rRNA and for large portions of mouse and human
; TITLE: 16S mitochondrial rRNAs
; JOURNAL: Nucleic Acids Research
; VOLUME: 9
; PAGES: 4303-4324
; DATE: 1981
; RELEVANT RESIDUES IN SEQ ID NO: 223 :FROM 1 TO 10
US-08-173-489C-223

```

```

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 9 TCGCCCTTC 18
   |||||
Db 10 TCCCTTC 1

```

```

RESULT 25
US-08-722-187-44
; Sequence 44, Application US/08722187
; Patent No. 595274
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/722,187
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-722-187-44

```

```

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 6 TCATCGCCCC 15
   |||||
Db 1 TTATCGCCCC 10

```

RESULT 26

US-08-388-353-83/c

; Sequence 83, Application US/08388353

; Patent No. 6010895

; GENERAL INFORMATION:

; APPLICANT: Deacon, Nicholas J.

; APPLICANT: Learmont, Jennifer C.

; APPLICANT: McPhee, Dale A.

; APPLICANT: Crowe, Suzanne

; APPLICANT: Cooper, David

; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1

; NUMBER OF SEQUENCES: 800

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Scully, Scott, Murphy & Presser

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: New York

; COUNTRY: United States

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/388,353

; FILING DATE: 14-FEB-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Digiglio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 9606

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (516) 742-4343

; TELEFAX: (516) 742-4366

; TELEX: 230 901 SANS UR

; INFORMATION FOR SEQ ID NO: 83:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

US-08-388-353-83

```

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 CCACCTCATC 10
   |||||
Db 10 CCACCCCATC 1

```

```

RESULT 27
US-08-388-353-191/c
; Sequence 191, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.

```

```

; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser

```

STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/388,353
FILING DATE: 14-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9606
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-388-353-191

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
Db 10 CCACCTCTTC 1

RESULT 28
US-08-488-551B-83/c
Sequence 83, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353

FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-83

Query Match 32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
Db 10 CCACCTCATC 1

RESULT 29
US-08-488-551B-191/c
Sequence 191, Application US/08488551B
Patent No. 6015661
GENERAL INFORMATION:
APPLICANT: Nicholas J. Deacon
APPLICANT: Dale A. McPhee
APPLICANT: David Cooper
TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
NUMBER OF SEQUENCES: 841
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 GARDEN CITY PLAZA
CITY: GARDEN CITY
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM0284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PN3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 191:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid

```
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-191

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
Db 10 CCACCTCTTC 1

RESULT 30
PCT-US95-04712-44
; Sequence 44, Application PC/TUS9504712
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M
; APPLICANT: Beck, James J
; TITLE OF INVENTION: Detection of Fungal Pathogens Using the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04712
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/233,608
; FILING DATE: 04-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Walsh, Andrea C.
; REGISTRATION NUMBER: 34,988
; REFERENCE/DOCKET NUMBER: CGC 1739
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8666
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
; DESCRIPTION: Oligonucleotide primer OPE-12
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
PCT-US95-04712-44

Query Match      32.3%; Score 8.4; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 30;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 TCATGCCCC 15
Db 1 TTATGCCCC 10

RESULT 31
US-08-173-489C-60
; Sequence 60, Application US/08173489C
```

```
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 bases
; TYPE: Nucleic Acid
; STRANDEDNESS: single stranded
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: third strand derived from HER-2
; DESCRIPTION: sequence region in Seq ID No. 586124459
; HYPOTHETICAL: Yes
; ANTI-SENSE: No
; PUBLICATION INFORMATION:
; RELEVANT RESIDUES IN SEQ ID NO: 60 :FROM 1 TO 11
US-08-173-489C-60

Query Match      32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTTC 18
Db 2 TCTCCCTTC 11

RESULT 32
US-09-196-523-16/c
; Sequence 16, Application US/09196523A
; Patent No. 6248525
; GENERAL INFORMATION:
; APPLICANT: Nilsen, Timothy W.
; TITLE OF INVENTION: Method for Identifying and Inactivating Essential or
; TITLE OF INVENTION: Functional Genes
; FILE REFERENCE: ILI 130
; CURRENT APPLICATION NUMBER: US/09/196,523A
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: 60/079,851
; EARLIER FILING DATE: 1998-03-30
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 16
```

;
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
US-09-196-523-16

Query Match 32.3%; Score 8.4; DB 1; Length 11;
Best Local Similarity 90.0%; Pred. No. 34;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10
| | | | |
Db 11 CCACGTCATC 2

RESULT 33
US-08-441-887A-334/c
; Sequence 334, Application US/08441887A
; Patent No. 5837832
; GENERAL INFORMATION:
; APPLICANT: Chee, Mark
; APPLICANT: Cronin, Maureen T.
; APPLICANT: Fodor, Stephen P.A.
; APPLICANT: Huang, Xiaohua X.
; APPLICANT: Hubbell, Earl A.
; APPLICANT: Lipshutz, Robert J.
; APPLICANT: Lobban, Peter E.
; APPLICANT: Morris, Macdonald S.
; APPLICANT: Sheldon, Edward L.
; TITLE OF INVENTION: Arrays of Nucleic Acid Probes on
; TITLE OF INVENTION: Biological Chips
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/441,887A
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,312
; FILING DATE: 26-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/082,937
; FILING DATE: 25-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Liebeschuetz, Joseph O.
; REGISTRATION NUMBER: 37,505
; REFERENCE/DOCKET NUMBER: 018547-004160US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-326-2400
; TELEFAX: 650-326-2422
; INFORMATION FOR SEQ ID NO: 334:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (probe)
US-08-441-887A-334

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 17 TCCTAAGCAT 26
| | | | |
Db 11 TCCTCAGCAT 2

RESULT 34
US-09-043-149-54/c
; Sequence 54, Application US/09043149
; Patent No. 6355418
; GENERAL INFORMATION:
; APPLICANT: Schmidt, Gunter
; TITLE OF INVENTION: Chimeric Oligonucleotides and Uses Thereof in the
; TITLE OF INVENTION: Identification of Antisense Binding Sites
; FILE REFERENCE: 020600-272
; CURRENT APPLICATION NUMBER: US/09/043,149
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: PCT/GB96/02275
; PRIOR FILING DATE: 1996-09-13
; PRIOR APPLICATION NUMBER: GB 9518864.5
; PRIOR FILING DATE: 1995-09-14
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-09-043-149-54

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CCTTCCTAAG 23
| | | | |
Db 10 CTTTCCTAAG 1

RESULT 35
US-09-874-601-134/c
; Sequence 134, Application US/09874601
; Patent No. 6632057
; GENERAL INFORMATION:
; APPLICANT: LEWIN, ALFRED S.
; APPLICANT: SHAW, LYNN C.
; APPLICANT: GRANT, MARIA B.
; TITLE OF INVENTION: ADENO-ASSOCIATED VIRUS-DELIVERED RIBOZYME COMPOSITIONS AND METHODS
; TITLE OF INVENTION: THE TREATMENT OF RETINAL DISEASES
; FILE REFERENCE: 4300.014100
; CURRENT APPLICATION NUMBER: US/09/874,601
; CURRENT FILING DATE: 2001-05-01
; PRIOR APPLICATION NUMBER: 09/063,667
; PRIOR FILING DATE: 1998-04-21
; PRIOR APPLICATION NUMBER: 60/046,147
; PRIOR FILING DATE: 1997-05-09
; PRIOR APPLICATION NUMBER: 60/044,492
; PRIOR FILING DATE: 1997-04-21
; NUMBER OF SEQ ID NOS: 182
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 134
; LENGTH: 12
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: ().()
; OTHER INFORMATION: SYNTHETIC OLIGONUCLEOTIDE
US-09-874-601-134

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 15 CTTCTTAAGC 24
Db 12 CTTCTTAAGC 3

RESULT 36
PCT-US94-08023-3
; Sequence 3, Application PC/TUS9408023
; GENERAL INFORMATION:
; APPLICANT: de Kloet, Siwo R.
; TITLE OF INVENTION: Sex-Specific DNA Probe For Parrots,
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell, P.A.
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/08023
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/093,198
; FILING DATE: 15-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: FL20979-34
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
PCT-US94-08023-3

Query Match 32.3%; Score 8.4; DB 1; Length 12;
Best Local Similarity 90.0%; Pred. No. 38;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 TTCCTTAAGCA 25
Db 2 TTCCTTAAGCA 11

RESULT 37
US-08-796-899-16
; Sequence 16, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; PRIOR APPLICATION DATA:
; NUMBER OF SEQUENCES: 32

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-796-899-16
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCACCTCA 8
Db 2 CCACCTCA 9
RESULT 38
US-08-796-899-20
; Sequence 20, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; PRIOR APPLICATION DATA:
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994

```
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-796-899-20
;
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTCA 8
Db 2 CCACCTCA 9

;
; RESULT 39
; US-08-796-899-21
; Sequence 21, Application US/08796899
; Patent No. 6160202
; GENERAL INFORMATION:
; APPLICANT: BUSTOS, Mauricio M
; APPLICANT: CHERN, Maw-Sheng
; TITLE OF INVENTION: MODIFICATION OF SEED CROPS WITH
; TITLE OF INVENTION: TRANSCRIPTION FACTORS
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/796,899
; FILING DATE: 06-FEB-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/319,544
; FILING DATE: 07-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-796-899-21
;
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Meuth, Donna M
; REGISTRATION NUMBER: 36,607
; REFERENCE/DOCKET NUMBER: 028754-005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6620
; TELEFAX: (703) 836-2021
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-796-899-20
;
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

;
; RESULT 40
; US-09-534-366A-20/c
; Sequence 20, Application US/09534366A
; Patent No. 6759195
; GENERAL INFORMATION:
; APPLICANT: Bentley, William E.
; APPLICANT: Gill, Ryan T.
; TITLE OF INVENTION: Method of Differential Display of Prokaryotic Messenger
; TITLE OF INVENTION: RNA by RTPCR
; FILE REFERENCE: Bentley et al., Method of . . .
; CURRENT APPLICATION NUMBER: US/09/534,366A
; CURRENT FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: PROV 60/126,038
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 20
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthesized
;
US-09-534-366A-20
;
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCATCGCC 13
Db 10 TCATCGCC 3

;
; RESULT 41
; US-09-442-054A-69
; Sequence 69, Application US/09442054A
; Patent No. 6770738
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Buchardt, Ole
; APPLICANT: Egholm, Michael
; APPLICANT: Berg, Rolf H.
; APPLICANT: Mollegaard, Neils E.
; TITLE OF INVENTION: Higher Order Structure And Binding Of Peptide Nucleic Acids
; FILE REFERENCE: ISIS4290
; CURRENT APPLICATION NUMBER: US/09/442,054A
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 08/471,907
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/054,363
; PRIOR FILING DATE: 1993-04-26
; PRIOR APPLICATION NUMBER: PCT/EP92/01219
; PRIOR FILING DATE: 1992-05-19
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 69
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: No. 6770738el Sequence
;
US-09-442-054A-69
;
Query Match 30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



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QY      13 CCCTTCCT 20
Db      1 CCCTTCCT 8

RESULT 42
US-09-941-042C-3
; Sequence 3, Application US/09941042C
; Patent No. 6911541
; GENERAL INFORMATION:
; APPLICANT: Conkling, Mark A.
; TITLE OF INVENTION: TRANSGENIC PLANTS CONTAINING MOLECULAR DECOYS THAT ALTER PROTEIN
; FILE OF INVENTION: THEREIN
; FILE REFERENCE: 5051-471WO
; CURRENT APPLICATION NUMBER: US/09/941,042C
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 60/229,198
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic oligonucleotide
US-09-941-042C-3

Query Match      30.8%; Score 8; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 CCACCTCA 8
Db      2 CCACCTCA 9

RESULT 43
US-08-196-103A-9
; Sequence 9, Application US/08196103A
; Patent No. 5672472
; GENERAL INFORMATION:
; APPLICANT: Ecker, David J.
; APPLICANT: Anderson, Kevin
; APPLICANT: Bruice, Thomas A.
; APPLICANT: Davis, Peter
; APPLICANT: Driver, Vickie
; APPLICANT: Hanecak, Ronnie C.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Vickers, Timothy A.
; TITLE OF INVENTION: Synthetic Unrandomization of Oligomer
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5672472ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,103A
; FILING DATE: February 22, 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 749,000
; FILING DATE: 23-AUG-1991

QY      13 CCCTTCCT 20
Db      1 CCCTTCCT 8

RESULT 44
US-08-357-396-9
; Sequence 9, Application US/08357396
; Patent No. 5698391
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; APPLICANT: Ecker, David J.
; APPLICANT: Anderson, Kevin
; APPLICANT: Bruice, Thomas A.
; APPLICANT: Davis, Peter
; APPLICANT: Driver, Vickie
; APPLICANT: Freier, Susan, M.
; APPLICANT: Hanecak, Ronnie C.
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Yogesh S. Sanghvi
; TITLE OF INVENTION: Improved Methods for Synthetic Unrandomization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5698391ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,396
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 749,000
; FILING DATE: 23-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 196,103
; FILING DATE: 22-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
```

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ATTORNEY/AGENT INFORMATION:
NAME: Gaumont, Rebecca R.
REGISTRATION NUMBER: 35,152
REFERENCE/DOCKET NUMBER: ISIS-0678
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
US-08-196-103A-9

Query Match      30.8%; Score 8; DB 1; Length 11;
Best Local Similarity 62.5%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCCT 20
Db      1 CCCUCCU 8

RESULT 44
US-08-357-396-9
; Sequence 9, Application US/08357396
; Patent No. 5698391
; GENERAL INFORMATION:
; APPLICANT: Philip Dan Cook
; APPLICANT: Ecker, David J.
; APPLICANT: Anderson, Kevin
; APPLICANT: Bruice, Thomas A.
; APPLICANT: Davis, Peter
; APPLICANT: Driver, Vickie
; APPLICANT: Freier, Susan, M.
; APPLICANT: Hanecak, Ronnie C.
; APPLICANT: Vickers, Timothy A.
; APPLICANT: Wyatt, Jacqueline
; APPLICANT: Yogesh S. Sanghvi
; TITLE OF INVENTION: Improved Methods for Synthetic Unrandomization
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 5698391ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/357,396
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 749,000
; FILING DATE: 23-AUG-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 196,103
; FILING DATE: 22-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ralph, Rebecca L.
; REGISTRATION NUMBER: 35,152
; REFERENCE/DOCKET INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
```

; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA (genomic)
 US-08-357-396-9

Query Match 30.8%; Score 8; DB 1; Length 11;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20
 Db 1 CCCUCCU 8

RESULT 45
 US-08-386-141-9
 ; Sequence 9, Application US/08386141
 ; Patent No. 5747253
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker, David J.
 ; APPLICANT: Davis, Peter
 ; APPLICANT: Vickers, Timothy A.
 ; TITLE OF INVENTION: COMBINATORIAL OLIGOMER
 ; TITLE OF INVENTION: IMMUNOSORBANT SCREENING ASSAY FOR TRANSCRIPTION
 ; TITLE OF INVENTION: FACTORS AND OTHER BIOMOLECULE BINDING
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and
 ; ADDRESSEE: No. 5747253ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: U.S.A.
 ; ZIP: 19103

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/386,141
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/032,852
 ; FILING DATE: 16 MAR 1993
 ; APPLICATION NUMBER: US/07/749,000
 ; FILING DATE: 23-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Gaumond, Rebecca R.
 ; REGISTRATION NUMBER: 35,152
 ; REFERENCE/DOCKET NUMBER: ISIS-0653
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: RNA (genomic)
 US-08-386-141-9

Query Match 30.8%; Score 8; DB 1; Length 11;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20

Db 1 CCCUCCU 8
 |||::||:

RESULT 46
 US-08-227-180B-14
 ; Sequence 14, Application US/08227180B
 ; Patent No. 5866698
 ; GENERAL INFORMATION:
 ; APPLICANT: Ecker et al.
 ; TITLE OF INVENTION: Modulation of Gene Expression
 ; TITLE OF INVENTION: Through Interference with RNA Secondary Structure
 ; NUMBER OF SEQUENCES: 51
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Jane Massey Licata, Esq.
 ; STREET: 210 Lake Drive East, Suite 201
 ; CITY: Cherry Hill
 ; STATE: NJ
 ; COUNTRY: USA
 ; ZIP: 08002

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
 ; COMPUTER: IBM 486
 ; OPERATING SYSTEM: WINDOWS FOR WORKGROUPS
 ; SOFTWARE: WORDPERFECT 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/227,180B
 ; FILING DATE: April 13, 1994
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/518,929
 ; FILING DATE: May 4, 1990
 ; APPLICATION NUMBER: PCT/US91/02588
 ; FILING DATE: April 15, 1991
 ; APPLICATION NUMBER: 07/801,168
 ; FILING DATE: No. 5866698ember 20, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jane Massey Licata
 ; REGISTRATION NUMBER: 32,257
 ; REFERENCE/DOCKET NUMBER: ISIS-1420
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (215) 568-3100
 ; TELEFAX: (215) 568-3439
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; ANTI-SENSE: yes
 US-08-227-180B-14

Query Match 30.8%; Score 8; DB 1; Length 11;
 Best Local Similarity 62.5%; Pred. No. 40;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCCT 20
 Db 1 CCCUCCU 8

RESULT 47
 US-08-623-891-104
 ; Sequence 104, Application US/08623891
 ; Patent No. 5795778
 ; GENERAL INFORMATION:
 ; APPLICANT: Kenneth G. Draper
 ; TITLE OF INVENTION: METHOD AND REAGENT FOR
 ; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
 ; TITLE OF INVENTION: VIRUS REPLICATION
 ; NUMBER OF SEQUENCES: 115
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon

STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,891
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/238,200
FILING DATE:
APPLICATION NUMBER: US/07/987,133
FILING DATE:
APPLICATION NUMBER: 07/882,921
FILING DATE: May 14, 1992
APPLICATION NUMBER: 07/948,359
FILING DATE: September 18, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 200/209
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 104:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-623-891-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.8%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
Db 1 CCCCCUGCCU 11

RESULT 48
US-08-173-489C-355
Sequence 355, Application US/08173489C
Patent No. 5861244
GENERAL INFORMATION:
APPLICANT: WANG, C. -G.
APPLICANT: HEPBURN, A. G.
TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
NUMBER OF SEQUENCES: 365
CORRESPONDENCE ADDRESS:
ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
STREET: 510 EAST 73RD STREET,
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 355:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: double stranded
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
DESCRIPTION: p53 gene, nucleotides 1153-1163
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
AUTHORS: Harlow, E., Williamson, N M, Ralston, R,
AUTHORS: Helfman, D M, Adams T E.
TITLE: Molecular cloning and in
TITLE: vitro expression of a cDNA for human cellular
TITLE: tumor antigen p53
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
PAGES: 1601-1610
DATE: 1985
RELEVANT RESIDUES IN SEQ ID NO: 355 :FROM 1 TO 11
US-08-173-489C-355

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 CTCATCGCCCC 15
Db 1 CTCCTCTCCCC 11

RESULT 49
US-09-340-861-104
Sequence 104, Application US/09340861
Patent No. 6432704
GENERAL INFORMATION:
APPLICANT: Kenneth G. Draper
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
TITLE OF INVENTION: VIRUS REPLICATION
NUMBER OF SEQUENCES: 115
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/340,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/987,133

```
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-340-861-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
DB 1 CCCCCUGCCU 11

RESULT 50
US-09-634-262-104
; Sequence 104, Application US/09634262
; Patent No. 6440719
; GENERAL INFORMATION:
; APPLICANT: Kenneth G. Draper
; TITLE OF INVENTION: METHOD AND REAGENT FOR
; TITLE OF INVENTION: INHIBITING HERPES SIMPLEX
; TITLE OF INVENTION: VIRUS REPLICATION
; NUMBER OF SEQUENCES: 115
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/634,262
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/987,133
; FILING DATE:
; APPLICATION NUMBER: 07/882,921
; FILING DATE: May 14, 1992
; APPLICATION NUMBER: 07/948,359
; FILING DATE: September 18, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 200/209
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 104:
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 11
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-634-262-104

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 63.6%; Pred. No. 43;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 CGCCCTTCCT 20
DB 1 CCCCCUGCCU 11

RESULT 51
US-09-249-155A-240/c
; Sequence 240, Application US/09249155A
; Patent No. 6538173
; GENERAL INFORMATION:
; APPLICANT: Heber-Katz, Ellen
; TITLE OF INVENTION: Compositions and Methods for Wound
; TITLE OF INVENTION: Healing
; FILE REFERENCE: 00486.78503
; CURRENT APPLICATION NUMBER: US/09/249,155A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,737
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/097,937
; PRIOR FILING DATE: 1998-08-26
; PRIOR APPLICATION NUMBER: US 60/102,051
; PRIOR FILING DATE: 1998-09-28
; NUMBER OF SEQ ID NOS: 346
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 11
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-249-155A-240

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCCTAAGCA 25
DB 11 CATCATAAGCA 1

RESULT 52
5494663-21/c
; Patent No. 5494663
; APPLICANT: YAMADA, MASAOKI;FURUTANI, YASUJI;YAMAYOSHI, MICHIKO;
;NOTAKE, MITSURU;YAMAGISHI, JUNICHI
; TITLE OF INVENTION: TREATMENT OF MICROBIAL INFECTION WITH
; INTERLEUKIN 1 POLYPEPTIDES
; NUMBER OF SEQUENCES: 34
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/252,826
; FILING DATE: 02-JUN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 954,418
; FILING DATE: 30-SEP-1992
; APPLICATION NUMBER: 496,800
; FILING DATE: 21-MAR-1990
; APPLICATION NUMBER: 812,796
; FILING DATE: 23-DEC-1985
; SEQ ID NO:21:
; LENGTH: 11
5494663-21

Query Match 30.0%; Score 7.8; DB 1; Length 11;
Best Local Similarity 81.8%; Pred. No. 43;
```

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 TCATCGCCCT 16
|||||
Db 11 TCATCAGCCT 1

RESULT 53

US-10-129-192A-2/c

; Sequence 2, Application US/10129192A

; Patent No. 6908761

; GENERAL INFORMATION:

; APPLICANT: KATAOKA, Kohsuke

; TITLE OF INVENTION: TRANSCRIPTION ACTIVATOR

; FILE REFERENCE: Q69817

; CURRENT APPLICATION NUMBER: US/10/129,192A

; PRIOR FILING DATE: 2002-05-02

; PRIOR APPLICATION NUMBER: PCT/JP00/00841

; PRIOR FILING DATE: 2000-02-15

; PRIOR APPLICATION NUMBER: JP 1999-314335

; PRIOR FILING DATE: 1999-11-04

; NUMBER OF SEQ ID NOS: 21

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 13

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: Maf recognition element

US-10-129-192A-2

Query Match

Best Local Similarity 30.0%; Score 7.8; DB 1; Length 13;

Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 CTTCTAAGCA 25

Db 11 CTTAGTAAGCA 1

RESULT 54

US-08-675-816-14/c

; Sequence 14, Application US/08675816

; Patent No. 6171864

; GENERAL INFORMATION:

; APPLICANT: Coughlan, Sean J.

; APPLICANT: Winfrey, Jr., Ron J.

; TITLE OF INVENTION: CALRETICULIN AND CALNEXIN GENES AND PROMOTER REGIONS AND USES

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Seed and Berry

; STREET: 701 Fifth Ave. Suite 6300

; CITY: Seattle

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/675,816

; FILING DATE: 05-JUL-1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: No. 6171864tenburg, Carol

; REGISTRATION NUMBER: 39,317

; REFERENCE/DOCKET NUMBER: 750027.401

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206-622-4900

; TELEFAX: (206)-682-6031

; INFORMATION FOR SEQ ID NO: 14:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

US-08-675-816-14

Query Match

Best Local Similarity 29.2%; Score 7.6; DB 1; Length 10;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCATC 10

Db 10 YCAVTCATC 1

RESULT 55

US-08-468-352-53/c

; Sequence 53, Application US/08468352

; Patent No. 5856459

; GENERAL INFORMATION:

; APPLICANT: Frank, Bruce L.

; APPLICANT: Roberts, Peter C.

; APPLICANT: Goodchild, John

; APPLICANT: Craig, J. Charles

; APPLICANT: Mills, John S.

; APPLICANT: Slade, Andrew

; APPLICANT: Roberts, No. 58564591 A.

; APPLICANT: Jupp, Raymond

; TITLE OF INVENTION: OLIGONUCLEOTIDES SPECIFIC FOR HEPATITIS

; TITLE OF INVENTION: B VIRUS

; NUMBER OF SEQUENCES: 56

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Lappin & Kusmer

; STREET: 200 State Street

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/468,352

; FILING DATE:

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Kerner, Ann-Louise

; REGISTRATION NUMBER: 33,523

; REFERENCE/DOCKET NUMBER: HYZ-041

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-330-1300

; TELEFAX: 617-330-1311

; INFORMATION FOR SEQ ID NO: 53:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; HYPOTHETICAL: NO

; ANTI-SENSE: YES

US-08-468-352-53

Query Match

Best Local Similarity 28.5%; Score 7.4; DB 1; Length 10;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17

Db 10 TCGACCTT 2

```
RESULT 56
US-08-678-039A-5/c
; Sequence 5, Application US/08678039A
; Patent No. 5858662
; GENERAL INFORMATION:
; APPLICANT: Keating, Mark T.
; APPLICANT: Morris, Colleen A.
; TITLE OF INVENTION: Diagnosis of Williams Syndrome and
; TITLE OF INVENTION: Williams Syndrome Cognitive Profile by Analysis of the
; TITLE OF INVENTION: Presence or Absence of a LIM-Kinase Gene
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P.C.
; STREET: 555 Thirteenth Street, N.W., Suite 701 East
; CITY: Tower
; STATE: DC
; COUNTRY: U.S.A.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/678,039A
; FILING DATE: 10-JUL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Stephen A.
; REGISTRATION NUMBER: 38,609
; REFERENCE/DOCKET NUMBER: 2323-120A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-624-1589
; TELEFAX: 202-763-6031
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
US-08-678-039A-5

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
DB 9 CAACCTCAT 1

RESULT 57
US-08-173-489C-280
; Sequence 280, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
DB 9 CAACCTCAT 1

RESULT 58
US-08-265-484B-14/c
; Sequence 14, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
```

```
STATE: NEW YORK
COUNTRY: USA
ZIP: 10021.
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44Mb storage
COMPUTER: IBM PC/XT/AT
OPERATING SYSTEM: MS-DOS version 6.2
SOFTWARE: Wordperfect Version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,489C
FILING DATE: 22 DEC 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/968,436
FILING DATE: 29 OCT 1992
ATTORNEY/AGENT INFORMATION:
NAME: Handelman, Joseph H.
REGISTRATION NUMBER: 26,179
REFERENCE/DOCKET NUMBER: U9518-6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (attorney) (212) 708-1880
TELEFAX: (attorney) (212) 246-8959
INFORMATION FOR SEQ ID NO: 280:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 bases
TYPE: nucleic acid
STRANDEDNESS: single stranded
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: third strand derived from C. burnetii
DESCRIPTION: 16s region in Seq ID No. 5861244279
HYPOTHETICAL: yes
ANTI-SENSE: no
PUBLICATION INFORMATION:
RELEVANT RESIDUES IN SEQ ID NO: 280 :FROM 1 TO 10
US-08-173-489C-280

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
DB 1 CCCCTTCCT 9

RESULT 58
US-08-265-484B-14/c
; Sequence 14, Application US/08265484B
; Patent No. 5998193
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perriman, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing
; TITLE OF INVENTION: Arms, Stems And Loops, tRNA Embedded
; TITLE OF INVENTION: Ribozymes and Compositions Thereof
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,484B
; FILING DATE: 24-JUN-1994
```

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; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
; US-08-365-484B-14

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 TCGCCCTT 17
Db 9 TCCCCCTT 1

RESULT 59
US-08-388-353-82/c
; Sequence 82, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-84

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCAT 9
Db 9 CCACCCCAT 1

RESULT 61
US-08-388-353-188/c
; Sequence 188, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CACCTCAT 10
Db 10 CACCCCAT 2

RESULT 60
US-08-388-353-84/c
; Sequence 84, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-84

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCACCTCAT 9
Db 9 CCACCCCAT 1

RESULT 61
US-08-388-353-188/c
; Sequence 188, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELEPHONE: (516) 742-4366
; TELEX: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-188

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCTCTTCCT 2

RESULT 62
US-08-388-353-189/c
; Sequence 189, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELEPHONE: (516) 742-4366
; TELEX: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-190

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCTCTTCCT 2
```

```
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-189

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 9 CCTCTTCCT 1

RESULT 63
US-08-388-353-190/c
; Sequence 190, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-190

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
```



```
Db          10 CACCTCTTC 2

RESULT 64
US-08-388-353-192/c
; Sequence 192, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-192

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          1 CCACCTCAT 9
Db          9 CCACCTCTT 1

RESULT 65
US-08-388-353-280/c
; Sequence 280, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-192

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy          9 TCCTCCCTT 17
Db          10 TCCTCCCTT 2

RESULT 66
US-08-388-353-281/c
; Sequence 281, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
```

```

; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-281

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17
Db 9 TCGCCCTT 1

RESULT 67
US-08-488-551B-82/c
; Sequence 82, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 82:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-82

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
Db 9 CCACCTCAT 1

RESULT 69
US-08-488-551B-188/c
; Sequence 188, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon

```

```

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
Db 10 CACCTCATC 2

RESULT 68
US-08-488-551B-84/c
; Sequence 84, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4366
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-84

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCACCTCAT 9
Db 9 CCACCTCAT 1

RESULT 69
US-08-488-551B-188/c
; Sequence 188, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon

```

```

; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-188

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 10 CCTCTTCCT 2

RESULT 70
US-08-488-551B-189/c
; Sequence 189, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; MEDIUM TYPE: Floppy disk

```

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-488-551B-189

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. NO. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
Db 9 CCTCTTCCT 1

RESULT 71
US-08-488-551B-190/c
; Sequence 190, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994

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```
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 190:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-190

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATC 10
Db      10 CACCTCTTC 2

RESULT 72
US-08-488-551B-192/c
; Sequence 192, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 192:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-190

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CACCTCATC 10
Db      10 CACCTCTTC 2
```

```
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-192

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCACCTCAT 9
Db      9 CCACCTCTT 1

RESULT 73
US-08-488-551B-280/c
; Sequence 280, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 280:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-280

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      9 TCGCCCTT 17
Db      10 TCCCTCTT 2
```

RESULT 74
US-08-488-551B-281/c
; Sequence 281, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-281

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17
|||
Db 9 TCCCTT 1

RESULT 75
US-08-765-257A-14/c
; Sequence 14, Application US/08765257A
; Patent No. 6107078
; GENERAL INFORMATION:
; APPLICANT: Keese, Paul
; APPLICANT: Stapper, Marianne
; APPLICANT: Perrinan, Rhonda
; TITLE OF INVENTION: Ribozymes With Optimized Hybridizing Arms,
; TITLE OF INVENTION: Stems And Loops, tRNA Embedded Ribozymes
; TITLE OF INVENTION: and Compositions Thereof

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH, 1.44Mb
; COMPUTER: IBM PC
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,257A
; FILING DATE: June 24, 1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 45284
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 977 9550
; TELEFAX: 212 977 9809
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other Nucleic Acid
US-08-765-257A-14

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 TCGCCCTT 17
|||
Db 9 TCCCTT 1

RESULT 76
US-09-261-115-65
; Sequence 65, Application US/09261115
; Patent No. 6458584
; GENERAL INFORMATION:
; APPLICANT: MIRZABEKOV, ANDREI
; APPLICANT: GUSCHIN, DMITRY Y.
; APPLICANT: SHIK, VALENTINE
; APPLICANT: DROBYSHEV, ALEKSEI
; APPLICANT: FOTIN, ALEXANDER
; APPLICANT: YERSHOV, GENNADIY
; APPLICANT: LYSOV, YU
; TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT
; TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE
; TITLE OF INVENTION: PORTABLE AND REUSABLE
; FILE REFERENCE: 21416/90184
; CURRENT APPLICATION NUMBER: US/09/261,115
; CURRENT FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Customized
; OTHER INFORMATION: oligonucleotide
US-09-261-115-65

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CACCTCATC 10
| | | | |
Db 1 CTCCTCATC 9

RESULT 77

US-09-486-853-16
; Sequence 16, Application US/09486853
; Patent No. 6461871
; GENERAL INFORMATION:
; APPLICANT: KUBISTA, MIKAEL
; APPLICANT: SVANVIK, NICKE
; APPLICANT: WESTMAN, GUNNAR
; TITLE OF INVENTION: METHOD FOR THE PREPARATION OF A PROBE FOR NUCLEIC ACID HYBRIDIZATION
; FILE REFERENCE: GOTEFO29US
; CURRENT APPLICATION NUMBER: US/09/486,853
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: PCT/SE98/01580
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: SE 9703251-0
; PRIOR FILING DATE: 1997-05-09
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 10
; TYPE: DNA
; ORGANISM: synthetic construct
US-09-486-853-16

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 CCCCTTCCT 20
| | | | |
Db 1 CCTCTTCCT 9

RESULT 78

US-09-914-259-139
; Sequence 139, Application US/09914259
; Patent No. 6495336
; GENERAL INFORMATION:
; APPLICANT: Makowski, Lee
; APPLICANT: Hyman, Paul
; APPLICANT: Williams, Mark
; TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
; FILE REFERENCE: 8471-010-999
; CURRENT APPLICATION NUMBER: US/09/914,259
; CURRENT FILING DATE: 2000-11-21
; NUMBER OF SEQ ID NOS: 180
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Theoretical sequence designed to show proper and improper joining
US-09-914-259-139

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 18 CCTAAGCAT 26
| | | | |
Db 2 CCCAAGCAT 10

RESULT 79

US-09-301-721A-28
; Sequence 28, Application US/09301721A
; Patent No. 6506561
; GENERAL INFORMATION:
; APPLICANT: CHEVAL, Lydie
; APPLICANT: ELALOUP, Jean-Marc
; APPLICANT: VIRLON, Berangere
; TITLE OF INVENTION: MICROASSAY FOR SERIAL ANALYSIS OF GENE EXPRESSION AND
; FILE REFERENCE: 0846-0499-0X
; CURRENT APPLICATION NUMBER: US/09/301,721A
; CURRENT FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EPO 99400189.9
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:synthetic DNA
US-09-301-721A-28

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 GCCCCTTCC 19
| | | | |
Db 1 GTCCCTTCC 9

RESULT 80

US-09-508-753B-423
; Sequence 423, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiiji OHARA
; APPLICANT: Masanori WATAHIKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 423
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-423

Query Match 28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 TTCCTAAGC 24
| | | | |
Db 1 TACCTAAGC 9

RESULT 81

US-09-508-753B-457
; Sequence 457, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:

```

; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 457
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-457

```

```

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      16 TTCTTAAGC 24
      |||||
DB      2 TTCTTAAGC 10

```

```

RESULT 82
US-09-508-753B-464/c
; Sequence 464, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHAKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 464
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-464

```

```

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      16 TTCTTAAGC 24
      |||||
DB      9 TTCTTAAGC 1

```

```

RESULT 83
US-09-721-777-10/c
; Sequence 10, Application US/09721777
; Patent No. PP13279
; GENERAL INFORMATION:
; APPLICANT: Khanuja, Suman Preet Singh
; APPLICANT: Kumar, Sushil
; APPLICANT: Shasany, Ajit Kumar

```

```

; APPLICANT: Dhawan, Sunita
; APPLICANT: Darokar, Mahendra Pandurang
; APPLICANT: Naqvi, Ali Arif
; APPLICANT: Dhawan, Om Parkash
; APPLICANT: Singh, Anil Kumar
; APPLICANT: Patra, Nirmal Kumar
; APPLICANT: Bahl, Janak Raj
; APPLICANT: Bansal, Ram Prakash
; TITLE OF INVENTION: Mint Plant Named Saksham
; FILE REFERENCE: 033166-002
; CURRENT APPLICATION NUMBER: US/09/721,777
; CURRENT FILING DATE: 2000-11-27
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: OPT primer
US-09-721-777-10

```

```

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      15 CTTCTTAAG 23
      |||||
DB      10 CTTCTTAAG 2

```

```

RESULT 84
5256545-10
; Patent No. 5256545
; APPLICANT: BROWN, MICHAEL S.; GOLDSTEIN, JOSEPH L.; RUSSELL,
; DAVID W.; SUDHOF, THOMAS C.
; TITLE OF INVENTION: STEROL REGULATORY ELEMENTS
; NUMBER OF SEQUENCES: 42
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/425,852
; FILING DATE: 20-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 33,330
; FILING DATE: 30-MAR-1987
; APPLICATION NUMBER: 33,081
; FILING DATE: 30-MAR-1987
; SEQ ID NO:10
; LENGTH: 10
5256545-10

```

```

Query Match      28.5%; Score 7.4; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 45;
Matches      8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      18 CCTAAGCAT 26
      |||||
DB      1 CCTAAGCAT 9

```

```

RESULT 85
US-08-250-310-12
; Sequence 12, Application US/08250310
; Patent No. 5559005
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosch, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 5559005el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 E. Lincoln Ave

```

;
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,310
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/953,492
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Speer, Raymond M.
; REGISTRATION NUMBER: 26,810
; REFERENCE/DOCKET NUMBER: 185721A
; TELEPHONE: (908) 594-4481
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-250-310-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTCTTA 21
Db 3 CTTCTTA 9
RESULT 86
US-08-439-404-12
; Sequence 12, Application US/08439404
; Patent No. 5629171
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosek, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 5629171el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen, III
; STREET: 126 E. Lincoln Ave; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,404
; FILING DATE: 11-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 18572DA
; TELECOMMUNICATION INFORMATION:

;
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-439-404-12
Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTCTTA 21
Db 3 CTTCTTA 9
RESULT 87
US-08-507-598-3
; Sequence 3, Application US/08507598
; Patent No. 5834188
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDEON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESS: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,598
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "Apl MUTATION"
US-08-507-598-3

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 15 CTTCTTA 21
Db 3 CTTCTTA 9

RESULT 86
US-08-439-404-12
; Sequence 12, Application US/08439404
; Patent No. 5629171
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosek, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 5629171el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen, III
; STREET: 126 E. Lincoln Ave; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,404
; FILING DATE: 11-May-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 18572DA
; TELECOMMUNICATION INFORMATION:

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 CCTCATC 10


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Db      3  CCTCATC 9

RESULT 88
US-08-173-489C-303/c
; Sequence 303, Application US/08173489C
; Patent No. 5861244
; GENERAL INFORMATION:
; APPLICANT: WANG, C. -G.
; APPLICANT: HEPBURN, A. G.
; TITLE OF INVENTION: GENETIC SEQUENCE ASSAY USING DNA
; TITLE OF INVENTION: TRIPLE-STRAND FORMATION.
; NUMBER OF SEQUENCES: 365
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PROFILE DIAGNOSTIC SCIENCES, INC.,
; STREET: 510 EAST 73RD STREET,
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10021.
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44Mb storage
; COMPUTER: IBM PC/XT/AT
; OPERATING SYSTEM: MS-DOS version 6.2
; SOFTWARE: Wordperfect Version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/173,489C
; FILING DATE: 22 DEC 1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/968,436
; FILING DATE: 29 OCT 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Handelman, Joseph H.
; REGISTRATION NUMBER: 26,179
; REFERENCE/DOCKET NUMBER: U9518-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (attorney) (212) 708-1880
; TELEFAX: (attorney) (212) 246-8959
; INFORMATION FOR SEQ ID NO: 303:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double stranded
; TOPOLOGY: linear
; MOLECULE TYPE: genomic DNA
; DESCRIPTION: 16S rRNA gene from Chlamydia psittaci
; DESCRIPTION: (Accession # M13769) nucleotides 1181 to 1190
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Chlamydia psittaci
; PUBLICATION INFORMATION:
; AUTHORS: Weisburg, W G, Hatch, T P, Woese, C R.
; TITLE: Eubacterial Origin of
; TITLE: Chlamydiae
; JOURNAL: Journal of Bacteriology
; VOLUME: 167
; PAGES: 570-574
; DATE: 1986
; RELEVANT RESIDUES IN SEQ ID NO: 303 :FROM 1 TO 10
US-08-173-489C-303

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      14  CCTTCCT 20
        |||||
Db      10  CCTTCCT 4

RESULT 89
US-08-545-253A-12/c
; Sequence 12, Application US/08545253A
; Patent No. 5908978
; GENERAL INFORMATION:
; APPLICANT: O'Malley, David M.
; APPLICANT: Sederoff, Ronald R.
; APPLICANT: Grattapaglia, Dario
; APPLICANT: Henry V. Amerson
; APPLICANT: Phillip Wilcox
; APPLICANT: E. George Kuhlman
; TITLE OF INVENTION: METHODS FOR WITHIN FAMILY
; TITLE OF INVENTION: SELECTION IN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth D. Sibley
; STREET: Post Office Drawer 34009
; CITY: Charlotte
; STATE: No. 5908978th Carolina
; COUNTRY: U.S.A.
; ZIP: 28234
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,253A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sibley, Kenneth D.
; REGISTRATION NUMBER: 31,665
; REFERENCE/DOCKET NUMBER: 5051-281
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 881-3140
; TELEFAX: (919) 881-3175
; TELEX: 575102
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-545-253A-12

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      18  CCTAAGC 24
        |||||
Db      10  CCTAAGC 4

RESULT 90
US-08-507-750-3
; Sequence 3, Application US/08507750
; Patent No. 5932716
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, T. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSEE: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
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;
;
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,750
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "APl MUTATION"
;
US-08-507-750-3
Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CCTCATC 10
Db 3 CCTCATC 9

RESULT 91
US-08-905-567-1
; Sequence 1, Application US/08905567
; Patent No. 6004750
; GENERAL INFORMATION:
; APPLICANT: Frank-Kamenetskii, Maxim D.
; APPLICANT: Veselkov, Alexei G.
; APPLICANT: Demidov, Vadim V.
; TITLE OF INVENTION: Nucleic Acid Clamps
; FILE REFERENCE: BU-03172
; CURRENT APPLICATION NUMBER: US/08/905,567
; CURRENT FILING DATE: 1997-08-04
; EARLIER APPLICATION NUMBER: 08/546,346
; EARLIER FILING DATE: 1995-10-20
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;
US-08-905-567-1
Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 CCCCTTC 18
Db 2 CCCCTTC 8

RESULT 92
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```
US-08-388-353-193/C
; Sequence 193, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
;
US-08-388-353-193
Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTC 7
Db 8 CCACCTC 2

RESULT 93
US-08-388-353-194/C
; Sequence 194, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
```

```
;
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-194

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTC 7
Db 7 CCACCTC 1

RESULT 94
US-08-388-353-210
; Sequence 210, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-210

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 3 CACCTCA 9

RESULT 96
US-08-388-353-212
; Sequence 212, Application US/08388353
; Patent No. 6010895
```

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-210

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 4 CACCTCA 10

RESULT 95
US-08-388-353-211
; Sequence 211, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-211

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 3 CACCTCA 9

RESULT 96
US-08-388-353-212
; Sequence 212, Application US/08388353
; Patent No. 6010895
```

```
;
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-212

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 2 CACCTCA 8
|||||

RESULT 97
US-08-388-353-213
; Sequence 213, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-212

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CACCTCA 8
Db 2 CACCTCA 8
|||||

RESULT 98
US-08-388-353-289/c
; Sequence 289, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-388-353-213
```

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; MOLECULE TYPE: DNA (genomic)
US-08-388-353-289

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCC 19
Db      10 CCCTTCC 4

RESULT 99
US-08-388-353-290/c
; Sequence 290, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 291:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-291

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCC 19
Db      8 CCCTTCC 2

RESULT 101
US-08-388-353-292/c
; Sequence 292, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
; APPLICANT: McPhee, Dale A.
; APPLICANT: Crowe, Suzanne
; APPLICANT: Cooper, David
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 800
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Scully, Scott, Murphy & Presser
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/388,353
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 290:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-290

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 CCCTTCC 19
Db      9 CCCTTCC 3

RESULT 100
US-08-388-353-291/c
; Sequence 291, Application US/08388353
; Patent No. 6010895
; GENERAL INFORMATION:
; APPLICANT: Deacon, Nicholas J.
; APPLICANT: Learmont, Jennifer C.
```

```
; FILING DATE: 14-FEB-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: DIGIGLIO, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9606
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-388-353-292

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 CCCTTCC 19
Db      7 CCCTTCC 1

RESULT 102
US-08-488-551B-193/c
; Sequence 193, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 193:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-388-353-292

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      13 CCCTTCC 19
Db      7 CCCTTCC 1

RESULT 103
US-08-488-551B-194/c
; Sequence 194, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 194:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-194

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      7 CCACCTC 1

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-193

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      8 CCACCTC 2

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-193

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCACCTC 7
Db      7 CCACCTC 1
```

RESULT 104

US-08-488-551B-210
; Sequence 210, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 210:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-210

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
Db 4 CACCTCA 10

RESULT 105

US-08-488-551B-211
; Sequence 211, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:

ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PM0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PM3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGILIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 211:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-211

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
Db 3 CACCTCA 9

RESULT 106

US-08-488-551B-212
; Sequence 212, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,551B

```

; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 212:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-212

```

```

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 CACCTCA 8
Db      2 CACCTCA 8

```

```

RESULT 107
US-08-488-551B-213
; Sequence 213, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 213:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-213

```

```

Query Match      26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 CACCTCA 8
Db      1 CACCTCA 7

```

```

RESULT 108
US-08-488-551B-289/c
; Sequence 289, Application US/08488551B
; Patent No. 6015661
; GENERAL INFORMATION:
; APPLICANT: Nicholas J. Deacon
; APPLICANT: Dale A. McPhee
; APPLICANT: David Cooper
; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
; NUMBER OF SEQUENCES: 841
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 11530-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/488,551B
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PM3864 (AU)
; FILING DATE: 14-FEB-1994
; APPLICATION NUMBER: PM4002 (AU)
; FILING DATE: 21-FEB-1994
; APPLICATION NUMBER: PN0284 (AU)
; FILING DATE: 23-DEC-1994
; APPLICATION NUMBER: US 08/388,353
; FILING DATE: 14-FEB-1995
; APPLICATION NUMBER: PN3021/95
; FILING DATE: 17-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FRANK S. DIGIGLIO
; REFERENCE/DOCKET NUMBER: 9606Z
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 289:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-488-551B-289

```


Query Match 26.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCC 19
 Db 10 CCCTTCC 4

RESULT 109
 US-08-488-551B-290/c
 ; Sequence 290, Application US/08488551B
 ; Patent No. 6015661
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas J. Deacon
 ; APPLICANT: Dale A. McPhee
 ; APPLICANT: David Cooper
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 ; NUMBER OF SEQUENCES: 841
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,551B
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PM3864 (AU)
 ; FILING DATE: 14-FEB-1994
 ; APPLICATION NUMBER: PM4002 (AU)
 ; FILING DATE: 21-FEB-1994
 ; APPLICATION NUMBER: PM0284 (AU)
 ; FILING DATE: 23-DEC-1994
 ; APPLICATION NUMBER: US 08/388,353
 ; FILING DATE: 14-FEB-1995
 ; APPLICATION NUMBER: PM3021/95
 ; FILING DATE: 17-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FRANK S. DIGIGLIO
 ; REFERENCE/DOCKET NUMBER: 96062
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 290:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-488-551B-290

Query Match 26.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCC 19
 Db 9 CCCTTCC 3

RESULT 110
 US-08-488-551B-291/c
 ; Sequence 291, Application US/08488551B

Patent No. 6015661
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas J. Deacon
 ; APPLICANT: Dale A. McPhee
 ; APPLICANT: David Cooper
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 ; NUMBER OF SEQUENCES: 841
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.
 ; ZIP: 11530-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/488,551B
 ; FILING DATE: 07-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PM3864 (AU)
 ; FILING DATE: 14-FEB-1994
 ; APPLICATION NUMBER: PM4002 (AU)
 ; FILING DATE: 21-FEB-1994
 ; APPLICATION NUMBER: PM0284 (AU)
 ; FILING DATE: 23-DEC-1994
 ; APPLICATION NUMBER: US 08/388,353
 ; FILING DATE: 14-FEB-1995
 ; APPLICATION NUMBER: PM3021/95
 ; FILING DATE: 17-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FRANK S. DIGIGLIO
 ; REFERENCE/DOCKET NUMBER: 96062
 ; TELEPHONE: (516) 742-4343
 ; TELEFAX: (516) 742-4366
 ; INFORMATION FOR SEQ ID NO: 291:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA
 ; US-08-488-551B-291

Query Match 26.9%; Score 7; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCC 19
 Db 8 CCCTTCC 2

RESULT 111
 US-08-488-551B-292/c
 ; Sequence 292, Application US/08488551B
 ; Patent No. 6015661
 ; GENERAL INFORMATION:
 ; APPLICANT: Nicholas J. Deacon
 ; APPLICANT: Dale A. McPhee
 ; APPLICANT: David Cooper
 ; TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 ; NUMBER OF SEQUENCES: 841
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 ; STREET: 400 GARDEN CITY PLAZA
 ; CITY: GARDEN CITY
 ; STATE: NEW YORK
 ; COUNTRY: U.S.A.

ZIP: 11530-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,551B
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PM3864 (AU)
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: PM4002 (AU)
FILING DATE: 21-FEB-1994
APPLICATION NUMBER: PM284 (AU)
FILING DATE: 23-DEC-1994
APPLICATION NUMBER: US 08/388,353
FILING DATE: 14-FEB-1995
APPLICATION NUMBER: PM3021/95
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: FRANK S. DIGIGLIO
REFERENCE/DOCKET NUMBER: 9606Z
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 292:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-488-551B-292

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CCCTTCC 19
Db 7 CCCTTCC 1

RESULT 112
US-08-839-327-12
Sequence 12, Application US/08839327
Patent No. 601726
GENERAL INFORMATION:
APPLICANT: CONDER, MICHAEL;
APPLICANT: MCADA, PHYLLIS; RAMBOSEK, JOHN;
APPLICANT: REEVES, CHRISTOPHER
TITLE OF INVENTION: NOVEL BIOPROCESS FOR
TITLE OF INVENTION: PREPARING 7-ACA AND 7-ADAC
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIERMAN, MUSERLIAN AND
ADDRESSEE: LUCAS, LLP
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/839,327
FILING DATE: 17-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 439,404

FILING DATE: 11-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 250,310
FILING DATE: 27-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 953,492
FILING DATE: 06-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 777,833
FILING DATE: 15-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSERLIAN
REGISTRATION NUMBER: 19,683
REFERENCE/DOCKET NUMBER: 253.171-DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8000
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: genomic DNA
US-08-839-327-12

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCTCA 21
Db 3 CTTCTCA 9

RESULT 113
US-08-719-337-12/c
Sequence 12, Application US/08719337
Patent No. 6054634
GENERAL INFORMATION:
APPLICANT: O'Malley, David M.
APPLICANT: Sederoff, Ronald R.
APPLICANT: Grattapaglia, Dario
TITLE OF INVENTION: METHODS FOR WITHIN FAMILY SELECTION IN
TITLE OF INVENTION: WOODY PERENNIALS USING GENETIC MARKERS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 6054634th Carolina
COUNTRY: U.S.A.
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/719,337
FILING DATE: 25-SEP-1996
CLASSIFICATION: 047
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,567
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5051-247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 881-3140
TELEFAX: (919) 881-3175
TELEX: 575102

```
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-719-337-12

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CCTAAGC 24
DB 10 CCTAAGC 4

RESULT 114
US-09-340-781B-12
; Sequence 12, Application US/09340781B
; Patent No. 6071713
; GENERAL INFORMATION:
; APPLICANT: Conder, Michael J.
; APPLICANT: McAda, Phyllis
; APPLICANT: Rambosek, John
; APPLICANT: Reeves, Christopher D.
; TITLE OF INVENTION: No. 6071713el Bioprocess for Preparing 7-ACA and 7-ADAC
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John W. Wallen, III
; STREET: 126 E. Lincoln Ave; P.O. Box 2000
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/340,781B
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/439,404
; FILING DATE: 11-May-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W.
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 18572DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-09-340-781B-12

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCTCTA 21
DB 3 CTTCTCTA 9

RESULT 115
US-08-764-522A-3
; Sequence 3, Application US/08764522A
; Patent No. 6090544
; GENERAL INFORMATION:
; APPLICANT: HARADA, SHUN-ICHI
; APPLICANT: SAMPATH, T. K.
; APPLICANT: RODAN, GIDEON A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,522A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-126
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 SEQUENCE A MUTATION"
US-08-764-522A-3

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CCTCATC 10
DB 3 CCTCATC 9

RESULT 116
US-08-764-528-3
; Sequence 3, Application US/08764528
; Patent No. 6103491
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, K. T.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, CREATIVE BIOMOLECULES
; STREET: 45 SOUTH STREET
; CITY: HOPKINTON
; STATE: MA
; COUNTRY: USA
; ZIP: 01748
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,528
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: VITO, CHRISTINE C.
; REGISTRATION NUMBER: 39,061
; REFERENCE/DOCKET NUMBER: CRP-127
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 SEQUENCE A MUTATION"
US-08-764-528-3

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Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 CCTCATC 10
Db 3 CCTCATC 9

```

```

RESULT 117
US-08-872-859-3
; Sequence 3, Application US/08872859
; Patent No. 6110460
; GENERAL INFORMATION:
; APPLICANT: SAMPATH, T. K.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR IDENTIFYING
; TITLE OF INVENTION: MORPHOGEN ANALOGS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
; ADDRESSER: THIBEAULT
; STREET: 53 STATE STREET
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/872,859
; FILING DATE: 11-JUN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/507,750
; FILING DATE: 26-JUL-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: PITCHER, EDMUND R.
; REGISTRATION NUMBER: 27,829
; REFERENCE/DOCKET NUMBER: CRP-116
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)-248-7000
; TELEFAX: (617)-248-7100

```

```

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..10
; OTHER INFORMATION: /product= "AP1 MUTATION"
US-08-872-859-3

```

```

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY 4 CCTCATC 10
Db 3 CCTCATC 9

```

```

RESULT 118
US-08-522-384-24
; Sequence 24, Application US/08522384
; Patent No. 6110667
; GENERAL INFORMATION:
; APPLICANT: LOPEZ-NIETO, CARLOS E
; TITLE OF INVENTION: PROCESSES, APPARATUS AND COMPOSITIONS FOR
; TITLE OF INVENTION: CHARACTERIZING NUCLEOTIDE SEQUENCES
; FILE REFERENCE: 2458-4029
; CURRENT APPLICATION NUMBER: US/08/522,384
; CURRENT FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Primer
US-08-522-384-24

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Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 CCTCATC 10
Db 1 CCTCATC 7

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```

RESULT 119
US-09-030-156-27/c
; Sequence 27, Application US/09030156
; Patent No. 6207373
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; TITLE OF INVENTION: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 221/157
; CURRENT APPLICATION NUMBER: US/09/030,156
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-030-156-27

```

```

Query Match          26.9%; Score 7; DB 1; Length 10;

```

Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTCTCA 21
| | | | |
Db 10 CTTCTCA 4

RESULT 120

US-09-645-757-27/c
; Sequence 27, Application US/09645757
; Patent No. 6395493
; GENERAL INFORMATION:
; APPLICANT: Sosnowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE OF INVENTION: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/09/645,757
; CURRENT FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; TYPE: DNA
; LENGTH: 10
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-645-757-27

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 CTTCTCA 21
| | | | |
Db 10 CTTCTCA 4

RESULT 121

US-09-229-007A-81/c
; Sequence 81, Application US/09229007A
; Patent No. 6453242
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; FILE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/09/229,007A
; CURRENT FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; TYPE: DNA
; LENGTH: 10
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-09-229-007A-81

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCACCTC 7
| | | | |
Db 7 CCACCTC 1

RESULT 122

US-10-108-280-27/c

; Sequence 27, Application US/10108280

; Patent No. 6753148

US-09-508-753B-52/c
; Sequence 52, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHUKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 52
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-52

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CACCTCA 8
| | | | |
Db 7 CACCTCA 1

RESULT 123

US-09-508-753B-128/c
; Sequence 128, Application US/09508753B
; Patent No. 6544736
; GENERAL INFORMATION:
; APPLICANT: Akira SHIMAMOTO
; APPLICANT: Yasuhiro FURUICHI
; APPLICANT: Yuko SHIBATA
; APPLICANT: Hiroko FUNAKI
; APPLICANT: Eiji OHARA
; APPLICANT: Masanori WATAHUKI
; TITLE OF INVENTION: Method for Synthesizing cDNA from mRNA sample
; FILE REFERENCE: 00162/HG
; CURRENT APPLICATION NUMBER: US/09/508,753B
; CURRENT FILING DATE: 2000-06-16
; PRIOR APPLICATION NUMBER: JP 9/270324
; PRIOR FILING DATE: 1997-09-18
; NUMBER OF SEQ ID NOS: 472
; SEQ ID NO 128
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-508-753B-128

Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GCCCCTT 17
| | | | |
Db 10 GCCCCTT 4

RESULT 124

US-10-108-280-27/c

; Sequence 27, Application US/10108280

; Patent No. 6753148

```

; GENERAL INFORMATION:
; APPLICANT: Senowski, Ronald G.
; TITLE OF INVENTION: METHODS AND APPARATUS FOR DETERMINATION OF LENGTH
; FILE OF INVENTION: POLYMORPHISMS IN DNA
; FILE REFERENCE: DAVID B. MURPHY: Nanogen 256/229
; CURRENT APPLICATION NUMBER: US/10/108,280
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US/09/645,757
; PRIOR FILING DATE: 2000-08-24
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-108-280-27

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 CTTCTTA 21
Db 10 CTTCTTA 4

RESULT 125
US-10-113-424-81/c
; Sequence 81, Application US/10113424
; Patent No. 6785613
; GENERAL INFORMATION:
; APPLICANT: Eisenberg, Stephen P.
; APPLICANT: Case, Casey C.
; APPLICANT: Cox III, George N.
; APPLICANT: Jamieson, Andrew
; APPLICANT: Rebar, Edward J.
; APPLICANT: Sangamo Biosciences, Inc.
; TITLE OF INVENTION: Selection of Sites for Targeting by Zinc Finger
; FILE OF INVENTION: Proteins and Methods of Designing Zinc Finger Proteins
; TITLE OF INVENTION: to Bind to Preslected Sites
; FILE REFERENCE: 019496-001800US
; CURRENT APPLICATION NUMBER: US/10/113,424
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: US/09/229,007A
; PRIOR FILING DATE: 1999-01-12
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: soybean FAD2-1 cDNA target segment FAD 4
US-10-113-424-81

Query Match          26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCACCTC 7
Db 7 CCACCTC 1

RESULT 126
US-09-875-453B-32/c
; Sequence 32, Application US/09875453B
; Patent No. 6838556
; GENERAL INFORMATION:
; APPLICANT: Kim, Jungsu H. P.
; APPLICANT: Starr, Douglas B.
; APPLICANT: Tam, Albert W.
; APPLICANT: Laurance, Megan E.

```

```

; APPLICANT: Michelotti, Emil F.
; APPLICANT: Velligan, Mark D.
; APPLICANT: Latour, Derek R.
; APPLICANT: Thomas, Rita L.
; APPLICANT: Kongpachith, Ana
; APPLICANT: Sheppard, Liana T.
; APPLICANT: Lim, Moon Young
; APPLICANT: Bruice, Thomas W.
; TITLE OF INVENTION: PROMOTERS FOR REGULATED GENE EXPRESSION
; FILE REFERENCE: 54600-8135.US00
; CURRENT APPLICATION NUMBER: US/09/875,453B
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US 60/209,549
; PRIOR FILING DATE: 2000-06-06
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Vancomycin resistant enterococcus
US-09-875-453B-32

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Best Local Similarity 100.0%; Pred. No. 52;
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Db 7 TTCCTAA 1

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; Sequence 110, Application US/08956518A
; Patent No. 6875606
; GENERAL INFORMATION:
; APPLICANT: Leonard, Sherry
; APPLICANT: Freedman, Robert
; TITLE OF INVENTION: ALPHA-7 NICOTINIC RECEPTOR
; NUMBER OF SEQUENCES: 121
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MEDLEN & CARROLL, LLP
; STREET: 220 Montgomery Street, Suite 2200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,518A
; FILING DATE: 23-OCT-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: MacKnight, Kamrin T.
; REGISTRATION NUMBER: 38,230
; REFERENCE/DOCKET NUMBER: UTC-03042
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-705-8410
; TELEFAX: 415-397-8338
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-956-518A-110

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Query Match 26.9%; Score 7; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 20 TAAGCAT 26
| | | | |
Db 2 TAAGCAT 8

Search completed: May 9, 2006, 16:54:32
Job time : 0.001 secs

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